

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Jacobs, Kenneth  
McCoy, John M.  
LaVallie, Edward R.  
Racie, Lisa A.  
Treacy, Maurice  
Spaulding, Vikki  
Agostino, Michael J.  
Howes, Steven H.  
Fechtel, Kim
- (ii) TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES  
ENCODING THEM
- (iii) NUMBER OF SEQUENCES: 231
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Genetics Institute, Inc.  
(B) STREET: 87 CambridgePark Drive  
(C) CITY: Cambridge  
(D) STATE: MA  
(E) COUNTRY: U.S.A.  
(F) ZIP: 02140
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Sprunger, Suzanne A.  
(B) REGISTRATION NUMBER: 41,323
- (ix) TELECOMMUNICATION INFORMATION:  
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2043 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTGAATGCC	CATGCGCAC	CCACAGCTCG	CGCTCCTGCA	AGTGTTCCTT	CTGGTGTTC	60
CCGATGGCGT	CCGGCCTCAG	CCTCTTCCT	CCCCATCAGG	GGCAGTGCCC	ACGTCTTTGG	120
AGCTGCAGCG	AGGGACGGAT	GGCGGAACCC	TCCAGTCCCC	TTCAGAGGCG	ACTGCAACTC	180
GCCCGGCCGT	GCCTGGACTC	CCTACAGTGG	TCCCTACTCT	CGTACTCC	TGGCCCCCTG	240
GGAATAGGAC	TGTGGACCTC	TTCCAGTCT	TACCGATCTG	TGTCTGTGAC	TTGACTCCTG	300
GAGCCTGCGA	TATAAATTGC	TGCTGCGACA	GGGACTGCTA	TCTTCTCCAT	CCGAGGACAG	360
TTTCTCTCTT	CTGCCTTCCA	GGCAGCGTAA	GGTCTTCAAG	CTGGGTTTGT	GTAGACAACT	420
CTGTTATCTT	CAGGAGTAAT	TCCCCGTTC	CTTCAAGAGT	TTTCATGGAT	TCTAATGGAA	480
TCAGGCAGTT	TTGTGTCCAT	GTGAACAACT	CAAACCTAAA	CTATTTCAG	AAGCTTCAAA	540
AGGTCAATGC	AACCAACTTC	CAGGCCCTGG	TTGCAGAGTT	TGGAGGCGAA	TCAATCACTT	600
CAACATTCCA	AACTCAATCA	CCACCATCTT	TTTACAGGGC	CGGGGACCCC	ATTCTTACTT	660
ACTTCCCCAA	GTGGTCTGTA	ATAAGCTTGC	TGAGACAACC	TGCAGGAGTT	GGAGCTGGGG	720
GACTCTGTGC	TGAAAGCAAT	CCTGCAGGTT	TCCTAGAGAG	TAAAAGTACA	ACTTGCACTC	780
GTTTTTTTCA	AGAACCTGGC	TAGTAGCTGT	ACCTTGGAAT	CAGCCCTCAA	TGCTGCCTCT	840
TACTATAACT	TCACAGTCTT	AAAGGTTC	AGAAGCATGA	CTGATCCACA	GAATATGGAG	900
TTCCAGGTT	CTGTAATACT	TACCTCACAG	GCTAATGCTC	CTCTGTGGC	TGGAAACACT	960
TGTCAGAATG	TAGTTTCTCA	GGTCACCTAT	GAGATAGAGA	CCAATGGGAC	TTTTGGAATC	1020
CAGAAAGTTT	CTGTCAAGTT	GGGACAAACC	AACCTGACTG	TTGAGCCAGG	CGCTTCTCTTA	1080
CAGCAACACT	TCATCTCTCG	CTTCAGGGCT	TTTCAACAGA	GCACAGCTGC	TTCTCTCACC	1140
AGTCTTAGAA	GTGGGAATCC	TGGCTATATA	GTGGGAAGC	CACTCTTGGC	TCTGACTGAT	1200
GATATAAGTT	ACTCAATGAC	CCTCTTACAG	AGCCAGGGTA	ATGGAAGTTG	CTCTGTTAAA	1260
AGACATGAAG	TGCAGTTTGG	AGTGAATGCA	ATATCTGGAT	GCAAGCTCAG	GTTGAAGAAG	1320
GCAGACTGCA	GCCACTTGCA	GCAGGAGATT	TATCAGACTC	TTCATGGAAG	GCCAGACCA	1380
GAGTATGTTG	CCATCTTTGG	TAATGCTGAC	CCAGCCCAGA	AAGGAGGGTG	GACCAGGATC	1440
CTCAACAGGC	ACTGCAGCAT	TTACAGTATA	AACTGTACTT	CCTGCTGTCT	CATACCAGTT	1500
TCCCTGGAGA	TCCAGGTATT	GTGGGCATAT	GTAGGTCTCC	TGTCCAACCC	GCAAGCTCAT	1560

GTATCAGGAG TTCGATTCTT ATACCACTGC CAGTCTATAC AGGATTCTCA GCAAGTTACA 1620  
 GAAGTATCTT TGACAACTCT TGTGAACTTT GTGGACATTA CCCAGAAGCC ACAGCCTCCA 1680  
 AGGGGCCAAC CCAAAATGGA CTGSAATGG CCATTCGACT TCTTCCCTT CAAAGTGGCA 1740  
 TTCAGCAGAG GAGTATTCTC TCAAAAATGC TCAGTCTCTC CCATCCTTAT CCTGTGCCTC 1800  
 TTAGAACTTG GAGTTCTCAA CCTAGAGACT ATGTGAAGAA AAGAAAATAA TCAGATTTCA 1860  
 GTTTTCCTTA TGAGAAACTC TGAGGCAGCC ACTTATCTTG GCTAAATAGA ACCTCACCTG 1920  
 CTCATGACCA GAGAGCATTT AGGATAATAG AGGACCTAAC TGAAGGAATC CTGTATATG 1980  
 AAAGGAGTTA TTTTAGAAAA GCAATAAAAA TATTTTATTC ATCATAAAAA AAAAAAAAAA 2040  
 AAA 2043

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Arg Thr Pro Gln Leu Ala Leu Gln Val Phe Phe Leu Val Phe  
 1 5 10 15  
 Pro Asp Gly Val Arg Pro Gln Pro Ser Ser Ser Pro Ser Gly Ala Val  
 20 25 30  
 Pro Thr Ser Leu Glu Leu Gln Arg Gly Thr Asp Gly Gly Thr Leu Gln  
 35 40 45  
 Ser Pro Ser Glu Ala Thr Ala Thr Arg Pro Ala Val Pro Gly Leu Pro  
 50 55 60  
 Thr Val Val Pro Thr Leu Val Thr Pro Ser Ala Pro Gly Asn Arg Thr  
 65 70 75 80  
 Val Asp Leu Phe Pro Val Leu Pro Ile Cys Val Cys Asp Leu Thr Pro  
 85 90 95  
 Gly Ala Cys Asp Ile Asn Cys Cys Cys Asp Arg Asp Cys Tyr Leu Leu  
 100 105 110  
 His Pro Arg Thr Val Phe Ser Phe Cys Leu Pro Gly Ser Val Arg Ser  
 115 120 125  
 Ser Ser Trp Val Cys Val Asp Asn Ser Val Ile Phe Arg Ser Asn Ser

03746783.122100

130	135	140
Pro Phe Pro Ser Arg Val Phe Met Asp Ser Asn Gly Ile Arg Gln Phe		
145	150	155
Cys Val His Val Asn Asn Ser Asn Leu Asn Tyr Phe Gln Lys Leu Gln		
	165	170
Lys Val Asn Ala Thr Asn Phe Gln Ala Leu Val Ala Glu Phe Gly Gly		
	180	185
Glu Ser Phe Thr Ser Thr Phe Gln Thr Gln Ser Pro Pro Ser Phe Tyr		
	195	200
Arg Ala Gly Asp Pro Ile Leu Thr Tyr Phe Pro Lys Trp Ser Val Ile		
	210	215
Ser Leu Leu Arg Gln Pro Ala Gly Val Gly Ala Gly Gly Leu Cys Ala		
	225	230
Glu Ser Asn Pro Ala Gly Phe Leu Glu Ser Lys Ser Thr Thr Cys Thr		
	245	250
Arg Phe Phe Gln Glu Pro Gly		
	260	

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1263 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAGCAGCTCA TCAACCCCTT TGGAGAGGAT GATGATGATT TTGAGACCAA CTGGATTGTC	60
GACAGGAATT TGCAGGTGTC CCTGTTGGCT GTGGATGAGA TGCACCAGGA CCTGCCTCGG	120
ATGGAGCCGG ACATGTACTG GAATAAGCCC GAGCCACAGC CCCCTACAC AGCTGCTTCC	180
GCCCAATTCC GTCGAGCCTC CTTTATGGGC TCCACCTTCA ACATCAGCCT GAACAAAGAG	240
GAGATGGAGT TCCAGCCCAA TCAGGAGGAC GAGGAGGATG CTCACGCTGG CATCATTTGGC	300
CGCTTCCTAG GCCTGCAGTC CCATGATCAC CATCTCCCA GGGCAAACCT AAGGACCAAA	360
CTACTGTGGC CCAAGAGGGA ATCCCTTCTC CACGAGGGCC TGCCCAAAAA CCACAAGGCA	420
GCCAAACAGA ACGTTAGGGG CCAGGAAGAC AACAAAGCCT GGAAGCTTAA GGCTGTGGAC	480
GCCTTCAAGT CTGCCCCACT GTATCAGAGG CCAGGCTACT ACAGTGCCCC ACAGACGCCC	540

CTCAGCCCCA CTCCCATGTT CTTCCCCCTA GAACCATCAG CGCCGTCAAA GCTTCACAGT 600  
 GTCACAGGCA TAGACACCAA AGACAAAAGC TTAAAGACTG TGAGTTCTGG GGCCAAGAAA 660  
 AGTTTGAAT TGCTCTCAGA GAGCGATGGG GCCTTGATGG AGCACCCAGA AGTATCTCAA 720  
 GTGAGGAGGA AAATGTGGA GTTTAACTTG ACGGATATGC CAGAGATCCC CGAAAATCAC 780  
 CTCAAAGAAC CTTTGGAACA ATCACCAACC AACATACACA CTACACTCAA AGATCACATG 840  
 GATCCTTATT GGGCCTTGGA AAACAGGGAT GAAGCACATT CCTAACCTGC TTCCTAATGG 900  
 GGATGCTTCG CCAGCCAGGT CCTCACCTGT GTGTACACCA GCAGGACACT GATCCAGTCA 960  
 CAGCCATACA GCTGTCCACA CTGAAGAACA TGTCCTACAA CAGCCTGAAT CAAATGGCTA 1020  
 GCTTAATAGA TAAAAATCCC AGACTACTTC AGCCTTTAAT GCCTTTTATT CATAAAAACT 1080  
 GTGAAAGCTA GACTGAACCA TTGAAACAT TTAAGTCTG CTCTGGATTC AGAGTCGGGA 1140  
 ACCCTTAGTT CTATCTGAAT CCAAGACAGC CACACCTTAG TATACTGCCC AAATAATGA 1200  
 GTTTAATAAA TACAAATACT CGTTAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1260  
 AAA 1263

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 261 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met His Gln Asp Leu Pro Arg Met Glu Pro Asp Met Tyr Trp Asn Lys  
 1 5 10 15  
 Pro Glu Pro Gln Pro Pro Tyr Thr Ala Ala Ser Ala Gln Phe Arg Arg  
 20 25 30  
 Ala Ser Phe Met Gly Ser Thr Phe Asn Ile Ser Leu Asn Lys Glu Glu  
 35 40 45  
 Met Glu Phe Gln Pro Asn Gln Glu Asp Glu Glu Asp Ala His Ala Gly  
 50 55 60  
 Ile Ile Gly Arg Phe Leu Gly Leu Gln Ser His Asp His His Pro Pro  
 65 70 75 80

[illegible]

(2) INFORMATION FOR SEQ ID NO:5:

(ii) MOLECULE TYPE: cDNA

CTTTGAGGGT	TTTTTGTTTT	TGTGTTTTTC	TAGGATTTC	TTGTGATGTT	TTGGTTTTGT	60
TTTTTGCTTT	TTGTTTAAGT	TGTGCTGACA	CCAAACACAT	CCAGTTTATA	ATCAGTACAT	120
TGGAAGCTG	GTATTGATGT	AGAACCAGTG	CATAACTTTT	TATGGGGTTT	TGTTATTGGT	180

TTTT TTTT TGA TAAAGTGTGA ATAAAAGGTA TGTTTACTCA TTTTCTCTGA ACACGTGTGT 240  
 GGTAATGTGC ATCATGACAA TTTCAGTGA AGGTGAGCTG GAGCTGGTTG GACTAATGAG 300  
 ACTGAGGAAG CAGCTTTTCC TACGATCTGC ATTATGTAAT CACAGGTCCA GAGAGCTTTA 360  
 TGGAAGCGGG AGAGGAGGAG CACTTACTCA TGTTGTATTT GTTAATGGAG GATGTCATCT 420  
 TTTCATAGAT GCTGGAACTA GAGTGCACCT GTTAGATGCT AAAGGTTTGA GCTTTACACA 480  
 AAATGCTTTC ATCTGTATTT GTTATTGTCT ACAATATATT TGAATTGGG GCAGCATATT 540  
 AAGATGTAAT GCCCTGTTAT GTCTGGAAAA AACTTGTTTT GCTTCTTCCA GGCAAAGGGC 600  
 ATTTTGTGGA TCAGTTTGAA CAGCTTCTCC ACCTTATTG GACAGTGATA AATTGAACCA 660  
 AGAGTGTAGA TTTACAAGTG TAACCTTCAA AAGAGGAAGA ACTATTGGG GTCTGTAGGT 720  
 AATGAACAGT CACACCAAAA TAGACTATGA TGCTTTTGTT AAGAAAGGTT TCATGTTTTA 780  
 GATATTTTCC GTGTCCTAAA TAATTTTCAA TAATCTATAA TCCCTAAAAT GCAATAAAAA 840  
 CTAGTATGTT TTCAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAA 894

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Cys	Ile	Met	Thr	Ile	Ser	Ser	Glu	Gly	Glu	Leu	Glu	Leu	Val	Gly
1				5					10					15	
Leu	Met	Arg	Leu	Arg	Lys	Gln	Leu	Phe	Leu	Arg	Ser	Ala	Leu	Cys	Asn
			20					25					30		
His	Arg	Ser	Arg	Glu	Leu	Tyr	Gly	Ser	Gly	Arg	Gly	Gly	Ala	Leu	Thr
			35				40					45			
His	Val	Val	Phe	Val	Asn	Gly	Gly	Cys	His	Leu	Phe	Ile	Asp	Ala	Gly
	50				55					60					
Thr	Arg	Val	His	Leu	Leu	Asp	Ala	Lys	Gly	Leu	Ser	Phe	Thr	Gln	Asn
65					70					75				80	
Val	Phe	Ile	Cys	Ile	Cys	Tyr	Cys	Leu	Gln	Tyr	Ile				
				85						90					

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 784 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCGGCCGCAG GTCTACTTGT GCGGAGCAGT CCAGCACAGC CTCACAGTGC AGAGCATGAG 60  
CTTTGGAGCC TGCCCCCACC CTAGCTTTGT GACCTTAAGT GAGCTACATA GCTTCTCATG 120  
TGTAACCTAC TCATCATAAT GGTTC TGACC TCAGTGGTTT GTTGTGTTCT AGGAAATGAT 180  
GCCAGTGAAT GCGTAGTCCC AGCCTCAGCA CAGGGGAGCC ACCTTGAAGC TCTCAAATAT 240  
CACTGTTGTG AATACAGAGA GGGAAAACCA ACTGTAACGT GCCACCCAAA TTTTTCAGA 300  
TTAATACATC ATTCATCAGA CTTCATTCGT GATCTCGAAG AGTGACATCA GTCTTCCTTG 360  
GAATATGAAG AGAATTTCTT TGGTTCCTCT TTTGCAITTC TATTTGATTT ATTTTATTTT 420  
ATTTTATTTT ATGTTTTTTG GTACAGAAAG CTCATTACTA GTCCTGTCCA GCAACGTGCC 480  
TCTCCTGGCC CTAGAGTTCT TGGAAATAGC CCAGGCCAAA GAGAAGGCCT TTCTCCCCAT 540  
GGTCAGCCAC ACGTTCCACA TGCGCACAGA GGAGTCTGAT GCCTCACAGG AGGGCGATGA 600  
CCTACCCAAG TCCTCAGCAA ACACCAGCCA TCCAAGCAG GATGACAGCC CCAAGTCCTC 660  
AGAAGAAACC ATCCAGCCCA AGGAGGGTGA CATCCCCAAG GCCCCAGAAG AAACCATCCA 720  
ATCCAAGAAG GAGGACCTCC CCAAGTCCTC GGAAAAAGCC ATCCAGCCCA AAGAGAGTAA 780  
CATC 784

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 140 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Lys Arg Ile Ser Leu Val Leu Leu Leu His Phe Tyr Leu Ile Tyr  
1 5 10 15



Phe Ile Leu Phe Tyr Phe Met Phe Phe Gly Thr Glu Ser Ser Leu Leu  
 20 25 30  
 Val Leu Ser Ser Asn Val Pro Leu Leu Ala Leu Glu Phe Leu Glu Ile  
 35 40 45  
 Ala Gln Ala Lys Glu Lys Ala Phe Leu Pro Met Val Ser His Thr Phe  
 50 55 60  
 His Met Arg Thr Glu Glu Ser Asp Ala Ser Gln Glu Gly Asp Asp Leu  
 65 70 75 80  
 Pro Lys Ser Ser Ala Asn Thr Ser His Pro Lys Gln Asp Asp Ser Pro  
 85 90 95  
 Lys Ser Ser Glu Thr Ile Gln Pro Lys Glu Gly Asp Ile Pro Lys  
 100 105 110  
 Ala Pro Glu Glu Thr Ile Gln Ser Lys Lys Glu Asp Leu Pro Lys Ser  
 115 120 125  
 Ser Glu Lys Ala Ile Gln Pro Lys Glu Ser Asn Ile  
 130 135 140

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 75 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 60  
 AAAAAAAAAA AAAAA 75

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 939 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CGAAGAAGTA GAAGCATCGA AAGCGTTGGA GAGGTGTTAC CGGAACGGCG GCGACAAGGG 60  
 TGTTCCCGAA CTAGAGTGGG GCATACATAA TCTTGCTGCT ATGCTTCGAA GCTGTAGTCT 120  
 GAATCAACCT AAGTTTAA CAGAAGGTGA ACCTCTGAGA TAGAAAATCA AGTATATT 180

AAAAGAAGGG ATGTGGGATC AAGGAGGACA GCCTTGGCAG CAGTGGCCCT TGAACCAGCA	240
ACAAATGGATG CAGTCATTCC AGCACCAACA GGATCCAAGC CAGATTGATT GGGCTGCATT	300
GGCCCAAGCT TGGATTGCCC AAAGAGAAGC TTCAGGACAG CAAAGCATGG TAGAACAACC	360
ACCAGGAATG ATGCCAAATG GACAAGATAT GTCTACAATG GAATCTGGTC CAAACAATCA	420
TGGGAATTTC CAAGGGGATT CAAACTTCAA CAGAAATGTG CAACCAGAAT GGGGAATGCA	480
TCAGCAACCC CCACACCCCC CTCCAGATCA GCCATGGATG CCACCAACAC CAGGCCCAAT	540
GGACATTGTT CCTCCTCTG AAGACAGCAA CAGTCAGGAC AGTGGGAAT TTGCCCTGTA	600
CAACAGGCAT ATATTTAACC AGAACAATCA CAACTTTGGT GGACCACCCG ATAATTTTGC	660
AGTGGGGCCA GTGAACCACT TTGACTATCA GGACCTCCAG GACCTCCAG ACCTCCCCAG	720
AATCGAAGAG AAAGGCCATC ATCAATCAGG GATCGTCAGC GTTCACCTAT TGCACCTCCT	780
GTGAAGCAGG AGCCTCCACA AATTGACGCA GTAAACGCA GGACTCTTCC CGCTTGGATT	840
CGCGAAGTTC TTGAAAAAAT GGAACGTGAA AAGCAGAAGA AATTGGAGAA AGAAAGAATG	900
GAACAACAAC GTTCACAATT GTCCAAAAAA AAAAAAAAAA	939

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Trp Asp Gln Gly Gly Gln Pro Trp Gln Gln Trp Pro Leu Asn Gln	
1 5 10 15	
Gln Gln Trp Met Gln Ser Phe Gln His Gln Gln Asp Pro Ser Gln Ile	
20 25 30	
Asp Trp Ala Ala Leu Ala Gln Ala Trp Ile Ala Gln Arg Glu Ala Ser	
35 40 45	
Gly Gln Gln Ser Met Val Glu Gln Pro Pro Gly Met Met Pro Asn Gly	
50 55 60	
Gln Asp Met Ser Thr Met Glu Ser Gly Pro Asn Asn His Gly Asn Phe	
65 70 75 80	
Gln Gly Asp Ser Asn Phe Asn Arg Met Trp Gln Pro Glu Trp Gly Met	

	85		90		95
His Gln Gln Pro Pro His Pro Pro Pro Asp Gln Pro Trp Met Pro Pro					
100			105		110
Thr Pro Gly Pro Met Asp Ile Val Pro Pro Ser Glu Asp Ser Asn Ser					
115		120		125	
Gln Asp Ser Gly Glu Phe Ala Pro Asp Asn Arg His Ile Phe Asn Gln					
130		135		140	
Asn Asn His Asn Phe Gly Gly Pro Pro Asp Asn Phe Ala Val Gly Pro					
145		150		155	160
Val Asn Gln Phe Asp Tyr Gln Asp Leu Gln Asp Leu Gln His Leu Pro					
	165		170		175
Arg Ile Glu Glu Lys Gly His His His Ser Gly Ile Val Ser Val His					
	180		185		190
Leu Leu His Phe Leu					
195					

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2343 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AGGAGAGCAG CCGGCAGCGC CTGGAGGCCCTGAGAGAGCT GCAATAAAGG AAGAAACAGA	60
ATATATGGA CTTCTGGCAG CAGAAAAACA TCAAGTTGAA GCCCTTAAAA ATATGCAACA	120
TCAAACCAA AGTTTATCCA TGCTTGACGA GATTCTTGAA GATGTAAGAA AGGCAGCGGA	180
TCGCTCGGAG GAAGAGATAG AGGAACATGC TTTTGACGAC AATAAATCAG TCAAGGGGGT	240
CAATTTTGAG GCAGTTCTGA GGGTGGAGGA AGAAGAGGCC AATTCTAAGC AAAATATAAC	300
AAAACGAGAA GTGGAGGATG ACTTGGGTCT TAGCATGCTG ATTGACTCCC AGAACAACCA	360
GTATATTTTG ACCAAGCCCA GAGATTCAAC CATCCCACGT GCAGATCACC ACTTTATAAA	420
GGACATTGTT ACCATAGGAA TGCTGTCCTT GCCTTGIGGC TGGCTATGTA CAGCCATAGG	480
ATGCGCTACA ATGTTTGTTT ATATTATTG TGGTGTACTT CTGGGACCTT CAGGACTAAA	540
TAGTATTAAG TCTATTGTGC AAGTGGAGAC ATTAGGAGAA TTTGGGGTGT TTTTACTCT	600

TTTTCTTGTT	GGCTTAGAAT	TTTCTCCAGA	AAAGCTAAGA	AAGGTGTGGA	AGATTTCCTT	660
ACAAGGGCCG	TGTTACATGA	CACTGTTAAT	GATTGCAITT	GGCTTGCTGT	GGGGGCATCT	720
CTTGGCGGATC	AAACCCACGC	AGAGCGTCTT	CATTTCACGC	TGTCTGTCCT	TGTCAGGCAC	780
ACCCCTCGTG	TCCAGGTTC	TCATGGGCAG	TGCTCGGGGT	GACAAAGAAG	GCGACATTGA	840
CTACAGCACC	GTGCTCCTCG	GCATGCTGGT	GACGCAGGAC	GTGCAGCTCG	GGCTCTTCAT	900
GGCCGTCATG	CCGACTCTCA	TACAGGCGGG	CGCCAGTGCA	TCTTCTAGCA	TTGTCGTGGA	960
AGTTCTCCGA	ATCCTGGTTT	TGATTGCTCA	GATTCTTTTT	TCACTAGCGG	CGGTTTTTCT	1020
TTTATGTCTT	GTTATAAAGA	AGTATCTCAT	TGGACCCAT	TATCGGAAGC	TGCACATGGA	1080
AAGCAAGGGG	AACAAAGAAA	TCCTGATCTT	GGGAATATCT	GCCTTTATCT	TCTTAATGTT	1140
AACGGTCACG	GAGCTGCTGG	ACGTCTCCAT	GGAGCTGGGC	TGTTTCCTGG	CTGGAGCGCT	1200
CGTCTCCTCT	CAGGGCCCCG	TGTCACCGA	GGAGATCGCC	ACCTCCATCG	AACCCATCCG	1260
CGACTTCCTG	GCCATCGTTT	TCTTCGCCCT	CATAGGGCTC	CACGTGTTCC	CCACGTTTGT	1320
GGCGTACGAG	CTCACGGTGC	TGGTGTTCCT	CACCTTGTC	GTGGTGTGTA	TGAAGTTTCT	1380
CCTGGCGGCG	CTGGTCTGCT	CTCTCATCT	GCCGAGGAGC	AGCCAGTACA	TCAAGTGGAT	1440
CGTCTCTGCG	GGGCTTGCCC	AGGTCAGCGA	GTTTTCTTTT	GTCCTGGGGA	GCCGGCGCGG	1500
AAGAGCGGGC	GTCATCTCTC	GGGAGGTGTA	CCTCCTTATA	CTGAGTGTGA	CCACGCTCAG	1560
CCTCTTGCTC	GCCCCGGTGC	TGTGGAGAGC	TGCAATCACG	AGGTGTGTGC	CCAGACCGGA	1620
GAGACGGTCC	AGCCTCTGAT	GGCTCGGAGA	TGATGGACCG	TGGAAGGGAA	GCGTCTGTGG	1680
GGAGTGAGCG	CTTAGATGGC	CAGCAGCTGC	TCCTTCTGGG	AAGCTCGCAC	CTTGGCAACA	1740
GAACAGCCCT	CTAGCAGAGC	GTCAGTGCAG	TCGTGTTATC	CCGGCTTTTA	CAGAATATTC	1800
TTGTCTCTATT	TTAGAAATTTT	CCGGAGTAGT	TTATTTGCAG	TCTGTTGATT	ATGTGCAGTA	1860
GACCCGGGAC	ACTGCGTTTT	ACCGATCACC	TGAAATGTGG	TGCCTGGATG	TGCCTTTTTT	1920
TTTTTTCCTT	GAAATTATTA	TTAATTTTCT	ATKKGAGATT	CATCAGTTCA	TAGTTTTTTT	1980
AGTAAAGAAG	CAAAATTAAG	AGGCTTTTAA	AAATGTACAA	CTTCAGAATT	ATAATCTGTT	2040
AGTCAAATAT	TTGTTATTAA	ACATTTCTGT	AATATGAAGT	TGTAATCCTG	GCCGTGAGCT	2100
TGGAAGCTTA	CTTTTGATTC	TTAAAGCCTA	TGTTTTCTAA	AATGAGACAA	ATACGGATGT	2160
CTATTTGCCT	TTTATTGTAA	CTTTTAAATG	AAATAATTTT	ATGTCATTTT	CTATTAGATA	2220
TATCACTTAA	AATATTTGGT	TTTAAATCAC	AAGAATATGT	ATTCTTTAAT	AAAGATAATT	2280
TATGATCATG	GTATAATTAA	TTGAAATTTA	TTAAATCTG	TTTTTATTAA	AAAAAAAAAA	2340

## (2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 524 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```

Met Glu Leu Leu Ala Ala Glu Lys His Gln Val Glu Ala Leu Lys Asn
1           5           10           15

Met Gln His Gln Asn Gln Ser Leu Ser Met Leu Asp Glu Ile Leu Glu
20           25           30

Asp Val Arg Lys Ala Ala Asp Arg Leu Glu Glu Glu Ile Glu Glu His
35           40           45

Ala Phe Asp Asp Asn Lys Ser Val Lys Gly Val Asn Phe Glu Ala Val
50           55           60

Leu Arg Val Glu Glu Glu Glu Ala Asn Ser Lys Gln Asn Ile Thr Lys
65           70           75           80

Arg Glu Val Glu Asp Asp Leu Gly Leu Ser Met Leu Ile Asp Ser Gln
85           90           95

Asn Asn Gln Tyr Ile Leu Thr Lys Pro Arg Asp Ser Thr Ile Pro Arg
100          105          110

Ala Asp His His Phe Ile Lys Asp Ile Val Thr Ile Gly Met Leu Ser
115          120          125

Leu Pro Cys Gly Trp Leu Cys Thr Ala Ile Gly Leu Pro Thr Met Phe
130          135          140

Gly Tyr Ile Ile Cys Gly Val Leu Leu Gly Pro Ser Gly Leu Asn Ser
145          150          155          160

Ile Lys Ser Ile Val Gln Val Glu Thr Leu Gly Glu Phe Gly Val Phe
165          170          175

Phe Thr Leu Phe Leu Val Gly Leu Glu Phe Ser Pro Glu Lys Leu Arg
180          185          190

Lys Val Trp Lys Ile Ser Leu Gln Gly Pro Cys Tyr Met Thr Leu Leu
195          200          205

Met Ile Ala Phe Gly Leu Leu Trp Gly His Leu Leu Arg Ile Lys Pro
210          215          220

Thr Gln Ser Val Phe Ile Ser Thr Cys Leu Ser Leu Ser Ser Thr Pro

```

225		230		235		240
Leu Val Ser Arg Phe	Leu Met Gly Ser Ala Arg Gly Asp Lys Glu Gly					
	245		250		255	
Asp Ile Asp Tyr Ser Thr Val Leu Leu Gly Met Leu Val Thr Gln Asp						
	260		265		270	
Val Gln Leu Gly Leu Phe Met Ala Val Met Pro Thr Leu Ile Gln Ala						
	275		280		285	
Gly Ala Ser Ala Ser Ser Ser Ile Val Val Glu Val Leu Arg Ile Leu						
	290		295		300	
Val Leu Ile Gly Gln Ile Leu Phe Ser Leu Ala Ala Val Phe Leu Leu						
	305		310		315	320
Cys Leu Val Ile Lys Lys Tyr Leu Ile Gly Pro Tyr Tyr Arg Lys Leu						
	325		330		335	
His Met Glu Ser Lys Gly Asn Lys Glu Ile Leu Ile Leu Gly Ile Ser						
	340		345		350	
Ala Phe Ile Phe Leu Met Leu Thr Val Thr Glu Leu Leu Asp Val Ser						
	355		360		365	
Met Glu Leu Gly Cys Phe Leu Ala Gly Ala Leu Val Ser Ser Gln Gly						
	370		375		380	
Pro Val Val Thr Glu Glu Ile Ala Thr Ser Ile Glu Pro Ile Arg Asp						
	385		390		395	400
Phe Leu Ala Ile Val Phe Phe Ala Ser Ile Gly Leu His Val Phe Pro						
	405		410		415	
Thr Phe Val Ala Tyr Glu Leu Thr Val Leu Val Phe Leu Thr Leu Ser						
	420		425		430	
Val Val Val Met Lys Phe Leu Leu Ala Ala Leu Val Leu Ser Leu Ile						
	435		440		445	
Leu Pro Arg Ser Ser Gln Tyr Ile Lys Trp Ile Val Ser Ala Gly Leu						
	450		455		460	
Ala Gln Val Ser Glu Phe Ser Phe Val Leu Gly Ser Arg Ala Arg Arg						
	465		470		475	480
Ala Gly Val Ile Ser Arg Glu Val Tyr Leu Leu Ile Leu Ser Val Thr						
	485		490		495	
Thr Leu Ser Leu Leu Leu Ala Pro Val Leu Trp Arg Ala Ala Ile Thr						
	500		505		510	
Arg Cys Val Pro Arg Pro Glu Arg Arg Ser Ser Leu						
	515		520			

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 324 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CGCAGCCCGG GCCATGCCCG ACGGCTGCTG ACCGCACGCA GGGGCCGGCC CCGAGGACAC	60
ATGCGGCGGC CTTTGCCGCC TCGCCCTGA CCTCTGCC TGTTCTCCAT GTTGCAATTC	120
TCGTCAGTTT CTCGGGCGGT GTAGTGCCG CTGCCACCAG AGCCGGCGGG GCATCGCGCT	180
GCTCATTCAT CCGGCCGCAC TTTCTTTTCC GTTTCCACCC ATCCCTTCCC ATTTCTTTCT	240
CCCTTTCCCC GCCAGCTTCG CATCCATCTC CCCCACCCCG TAACCCCTCC TGCTCCATC	300
CACCGGGGCT ATTGCCGCAA AAGA	324

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 550 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCTGAACATT TCAGAAATAC AGAAGTTGAA GCAGCAGCTT ATGCAGGTAG AGCGGGAAAA	60
GGCCATTCTT TTGGCCAACC TACAGGAGTC ACAGACACAG CTGGAACACA CCAAGGGGGC	120
ACTGACGGAG CAGCATGAGC GGGTGCACCG GCTCACAGAG CAGTCAATG CCATGAGGGG	180
CCTGCAAAGC AGCAAGGAGC TCAAGGCTGA GCTGGACGGG GAGAAGGGCG GGGACTCAGG	240
GGAGGAGGCC CATGACTATG AGGTGGACAT CAATGGTTTA GAGATCCTTG AATGCAAATA	300
CAGGGTGCCA GTAAGTGAGG TGATTGATCT GAAAGCTGAA ATTAAGGCCT TAAAGAGGAA	360
ATATAATAAA TCTGTAGAAA ACTACACTGA TGAGAAGGCC AAGTATGAGA GTAAAATCCA	420
GATGTATGAT GAGCAGGTGA CAAGCCTTGA GAAGACCACC AAGGAGAGTG GTGAGAAGAT	480
GGCCACATG GAGAAGGAGT TGCAAAAGAT GACCAGCATA GCCAACGAAA ATCACAGTAC	540
CCTTAATACG	550

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 170 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```

Met Gln Val Glu Arg Glu Lys Ala Ile Leu Leu Ala Asn Leu Gln Glu
1             5             10             15

Ser Gln Thr Gln Leu Glu His Thr Lys Gly Ala Leu Thr Glu Gln His
          20             25             30

Glu Arg Val His Arg Leu Thr Glu His Val Asn Ala Met Arg Gly Leu
          35             40             45

Gln Ser Ser Lys Glu Leu Lys Ala Glu Leu Asp Gly Glu Lys Gly Arg
          50             55             60

Asp Ser Gly Glu Glu Ala His Asp Tyr Glu Val Asp Ile Asn Gly Leu
          65             70             75             80

Glu Ile Leu Glu Cys Lys Tyr Arg Val Ala Val Thr Glu Val Ile Asp
          85             90             95

Leu Lys Ala Glu Ile Lys Ala Leu Lys Glu Lys Tyr Asn Lys Ser Val
          100            105            110

Glu Asn Tyr Thr Asp Glu Lys Ala Lys Tyr Glu Ser Lys Ile Gln Met
          115            120            125

Tyr Asp Glu Gln Val Thr Ser Leu Glu Lys Thr Thr Lys Glu Ser Gly
          130            135            140

Glu Lys Met Ala His Met Glu Lys Glu Leu Gln Lys Met Thr Ser Ile
          145            150            155            160

Ala Asn Glu Asn His Ser Thr Leu Asn Thr
          165            170

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(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 505 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TTCCATGAGT GAATTCATCC AAGGGCACGG GTTCAGCAAG GAAAAAAGGT TAACCGTGGT

60



TCCACCAGCA AAAAGAGATT GTCAGCAGCC TGTGCTCCG TACCGCCACA GTGTTACAA 120  
 CTAGCCGGGA GGCAAGACTG CCCAACTGTC AGTCTCTCCC TGAGGAGCAG 180  
 CCACATTCCA GCTCCCAGTG CGCCCTCTC CACTGTCTCT CCAAGCCTCC TCACCCCTAG 240  
 TCTTCATCTC CTGTGGACAA ACATCTGGGG TGGAAAGTTT GTAGCCACAC ACAGGATACT 300  
 GCCCAAGATC CAGCGGGTGT TTTCTTCTCG GTTGTTAGAT GTACAATTGG ATTAATGTCC 360  
 ATCGTTTTGG AAGACGAGAG AAAGTTGAGA AGAACACGAA GCACAGACCC TGATGTGATA 420  
 AAACATTTGT TGTTTCTCT GAGTCACAGA TAAACTTCTG CCATCAAATG GCTACAGTTC 480  
 ATTTAAATTT AAAAAAAAAA AAAAA 505

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 481 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGATACTGTA ATAAATAGGA GACAGCTACA GTGATCCAAC TAAACCAACA GGGGATTTC 60  
 ATCAGCACTT CCTGGTGTA ATCATGGTAC AGATTATTAA AGACACGAAT GAATTTAAAA 120  
 CATTTTTGAC AGCTCCCGGA CACAACTCG CAGTGGTTCA ATTTTCTTCG AAACGGTGIG 180  
 GTCCCTGCAA AAGGATGTTT CCTGTTTCC ATGAGCTGGC TGAACCTGT CATATCAAAA 240  
 CAATACCCAC ATTTAGATG TTCAAGAAAA GCCAGAAGGT AACCTATTTC TCAAGAATCA 300  
 AAAGAATAAT TTGCTGTTAT AGAAGTGGAT TCATGAGCAA CCTGATTTT GAGTTTGTG 360  
 GAGCCGATGC TAAAAAATTG GAAGCCAAGA CTCAGAATT AATGTAAGCT GATCTCCAAG 420  
 GCAAAATACA CTGTGTGACAT TTGAAAAGGC AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 480  
 A 481

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 107 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Val Gln Ile Ile Lys Asp Thr Asn Glu Phe Lys Thr Phe Leu Thr  
 1 5 10 15  
 Ala Ala Gly His Lys Leu Ala Val Val Gln Phe Ser Ser Lys Arg Cys  
 20 25 30  
 Gly Pro Cys Lys Arg Met Phe Pro Val Phe His Glu Leu Ala Glu Thr  
 35 40 45  
 Cys His Ile Lys Thr Ile Pro Thr Phe Gln Met Phe Lys Lys Ser Gln  
 50 55 60  
 Lys Val Thr Leu Phe Ser Arg Ile Lys Arg Ile Ile Cys Cys Tyr Arg  
 65 70 75 80  
 Ser Gly Phe Met Ser Asn Leu Ile Phe Glu Phe Cys Gly Ala Asp Ala  
 85 90 95  
 Lys Lys Leu Glu Ala Lys Thr Gln Glu Leu Met  
 100 105

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1864 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGCCAAAGAG GCCTATTCTT GTGTGCAATC AGTACCTTGA AGGCAGAACA TTCTGAATAA	60
AGTTGGAAAA AGAACAGCTT TGCTTTGCAA AGATTGATGA CAGACTGGTT CCTCAGAGGC	120
CTAGGCTACC CGTCACCCCT TTTCCAGAG CGAGGGCCTG GAATGAAGGC AGTTTATCCT	180
CTGTCCCTGG AGCCTGGGGT TTGCTTTGGC TCCTTGAGGT GGAAGAGACT AAGAGGGCAG	240
CTGCCCAGAG CAGCTGTGTG TACCTGGCTC CTCTCAGGCT TCCTGATCCC TTCCATTGCA	300
CTGCGCCTTA TCCCTCAGCC AGCCAGACAG CCTCCCTGCT CCTGACCAGC AGATACGTTT	360
CGGAGTGTTT GGTGTGGTTT TTGTGATGAG GGCAGCACGT GGTGGCCAAG GTGGCAAGCT	420
GAGTCTCACA GGCTCACTCC CTCGTTGGTT CCCTGTGGGA ATGSTATAGGC AGGCCARTA	480
AGCCATGCCC CAACACGTCC TCTCCTCCGG AGGAAGGGCC AGTGCCART TGARTCAGCA	540
GCTAGTCCAT AGCAGACCT TATAACTGTA AAGCCAGGCA TTGCCCATGA GCAGAGCTGG	600
AACCAGAGCT TCAGTCAGTA AGAGGGAGGA TTACCTTCAG GAGAAGGCAA GGAAGAAAAC	660
TGGCTGCTAT CTTTATAGTT CCACTGCCCT AACCAAGTGT CCACATTCTA AATGTGTAGT	720

GTCCATCCCT TATGTAATAG TGGTTTCCCG CCCAAAGTGA GACTTTCCTT TTAATTGGAG	780
AAGGGTATAG AGGTAGTCCA GGTGGGAACG CCAGAAGTGC TGATTGCCCA GCCATTGGGA	840
CCACCTGTTC TTGCCCCACT ACCCTCTAGT GGGAGGCCAA AGTAAAGGCT GGCTGGTGGG	900
TGTCGTGGA TTGAGGATGT GGCAGGGACT GGTCTCCCA CCTCCCTCTG GCCAAAGATG	960
GGCTTTGCCC GCTGTGTGCC TGTACCACC CACCAGCAGT CATGCCCTGG GCTTCCCAAA	1020
TGGAGAGGTA GCAGGCAACG TTTTAAAAA GAAAGAAAA AGGAAACTGT ATTGTGTCGG	1080
GGGAGGCGGG AGGAGATGA GGAAACGGTT TGSATTTTGT GTGTGGGAGG GTATTTTTTG	1140
GGGGTAGTTG TCTGTAACCT TCCTAAGTGC TTTTTCCT TTTCTTTTTT AAAGTAAGTT	1200
GCAGGCTTGT GCTTGGAAAA CCCAGGGGG ATGGGGGCA GAAACCTGAG GCTGCTGCC	1260
TTTATCTGCC TTCACGGTAC TGTCCCTTC CCCAGCTCC TCCCTGACCC CATGGGCCAG	1320
GCCTCAGACC TTCCAGCTAA CCGCTTCCCA TGAGCCACTA CTCTGATGTC AGCCTATAAC	1380
CAAAGSAGCT GGGGGGTCCA GGCCTGGTGA CCAACCTTC TCAGCCCACT CAATCAGGGT	1440
GCTCCCCACC TGCAGGCAGG AGSCAACACC CTATCTGCTA CCATCAGCCC CTTCCAGAGC	1500
CCATCTGCCC CGCCAGCCC TGCCCTGCC AGCCATACCC TGCTCTGCC CATCTGGGGG	1560
TGCCCTGCTC AGGGATGGG TGGCAGGGCT GTACCCAGCC TCCCTGGTAA GCAGAGACTC	1620
AAGAAACCTC TGGGGTCCTG TTTCTGCTC GTGTGATCCC AGGGGTGCAC ATGGGCCCCT	1680
TGGGTGTCTG AACAGAAGG CATGGGAGG AGGGCTGCAC CCCTGCAGTC TTAATCTGCT	1740
GGTGTAGCGG GCAGMTGCC ACTCCACCC CACCCTGCAC CGCGGGCTCC TGAGTCGGCA	1800
GATTAAGCAT TTTATAAATT GTATTTTAAA TACATGTTTT AAACCTGTCA AAAAAAAAAA	1860
AAAA	1864

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 102 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Val	Leu	Pro	Thr	Cys	Arg	Gln	Glu	Ala	Thr	Pro	Tyr	Leu	Leu	Pro	Ser
1				5					10					15	
Ala	Pro	Ser	Arg	Ala	His	Leu	Pro	Arg	Pro	Ala	Leu	Pro	Cys	Pro	Ala
			20					25					30		

Ile Pro Cys Ser Ala Pro Ser Gly Gly Ala Leu Leu Arg Asp Gly Leu  
 35 40 45

Ala Gly Leu Tyr Pro Ala Ser Leu Val Ser Arg Asp Ser Arg Asn Leu  
 50 55 60

Trp Gly Pro Val Phe Trp Ser Cys Asp Pro Arg Gly Ala His Gly Pro  
 65 70 75 80

Leu Gly Cys Leu Asn Arg Arg Ala Trp Glu Gly Gly Leu His Pro Cys  
 85 90 95

Ser Leu Thr Leu Leu Val  
 100

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1041 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AGCCCTCGTA CTGATTCCCA TCGTTGCATT TACAACTGCT ACACAAATGC CAGCACTCCA 60

TCGACATGAA GAAGAGAAAT TCTTCTTAAA TGCCAAAGGC CAGAAAGAAA CTTTACCCAG 120

CATATGGGAC TCACCTACCA AACAACTTTC TGTCGTTGTG CCTTCAAACA ATGAAGAAAA 180

ACGGTTGCCT GTGATGATGG ATGAAGCTCT GAGCTATGTA GAGAAGAGAC AGAAACGAGA 240

TCCTGCGTTC ACTTATGAAG TGATAGTAGT TGATGATGGC AGTAAAGATC AGACCTCAAA 300

GGTAGCTTTT AAATATTGCC AGAAATATGG AAGTGACAAA GTACGTGTGA TAACCTTGST 360

GAAGAATCGT GGAAAAGGTG GAGCGATTAG AATGGGTATA TTCAGTTCTC GAGGAGAAAA 420

GATCCTTATG GCAGATGCTG ATGGAGCCAC AAAGTTTCCA GATGTTGAGA AATTAGAAAA 480

GGGGCTAAAT GATCTACAGC CTGGCCTAA TCAATGGCT ATAGCATGTG GATCTCGAGC 540

TCATTAGAA AAAGAATCAA TTGCTCAGCG TTCTTACTTC CGTACTCTTC TCATGTIATGG 600

GTTCCACTTT CTGGTGTGGT TCCTTTGTGT CAAAGGAATC AGGGACACAC AGTGTGGGTT 660

CAAATTATTT ACTCGAGAAG GAGCTTCACG GACGTTTTC TCTTACACG TTGAACGATG 720

GGCATTGTAT GTAGAACTAG TGTACATAGC ACAGTTCTTT AAAATTCCAA TAGCAGAAAT 780

TGCTGTCAAC TGGACAGAAA TTGAAGGTTC TAAATTAGTT CCATTCTGGA GCTGGCTACA 840

AATGGGTAAA GACCTACTTT TTATACGACT TCGATATTTG ACTGGTGCCT GGAGGCTTGA 900

GCAAACTCGG AAAATGAATT AGGTTGTTTG CAGTCTTCAG TTGTGTTCTT ATGCTTCAGT 960  
 GTCACATTTC ATTTCATTTG AACTAAAAA TTTAAGTAAA GCTGAAATAA ACTTCTTGTC 1020  
 ATTGTCAAAA AAAAAAAAAA A 1041

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met	Pro	Ala	Leu	His	Arg	His	Glu	Glu	Lys	Phe	Phe	Leu	Asn	Ala	1	5	10	15	
Lys	Gly	Gln	Lys	Glu	Thr	Leu	Pro	Ser	Ile	Trp	Asp	Ser	Pro	Thr	Lys	20	25	30	
Gln	Leu	Ser	Val	Val	Val	Pro	Ser	Asn	Asn	Glu	Glu	Lys	Arg	Leu	Pro	35	40	45	
Val	Met	Met	Asp	Glu	Ala	Leu	Ser	Tyr	Val	Glu	Lys	Arg	Gln	Lys	Arg	50	55	60	
Asp	Pro	Ala	Phe	Thr	Tyr	Glu	Val	Ile	Val	Val	Asp	Asp	Gly	Ser	Lys	65	70	75	80
Asp	Gln	Thr	Ser	Lys	Val	Ala	Phe	Lys	Tyr	Cys	Gln	Lys	Tyr	Gly	Ser	85	90	95	
Asp	Lys	Val	Arg	Val	Ile	Thr	Leu	Val	Lys	Asn	Arg	Gly	Lys	Gly	Gly	100	105	110	
Ala	Ile	Arg	Met	Gly	Ile	Phe	Ser	Ser	Arg	Gly	Glu	Lys	Ile	Leu	Met	115	120	125	
Ala	Asp	Ala	Asp	Gly	Ala	Thr	Lys	Phe	Pro	Asp	Val	Glu	Lys	Leu	Glu	130	135	140	
Lys	Gly	Leu	Asn	Asp	Leu	Gln	Pro	Trp	Pro	Asn	Gln	Met	Ala	Ile	Ala	145	150	155	160
Cys	Gly	Ser	Arg	Ala	His	Leu	Glu	Lys	Glu	Ser	Ile	Ala	Gln	Arg	Ser	165	170	175	
Tyr	Phe	Arg	Thr	Leu	Leu	Met	Tyr	Gly	Phe	His	Phe	Leu	Val	Trp	Phe	180	185	190	
Leu	Cys	Val	Lys	Gly	Ile	Arg	Asp	Thr	Gln	Cys	Gly	Phe	Lys	Leu	Phe	195	200	205	

Thr	Arg	Glu	Ala	Ala	Ser	Arg	Thr	Phe	Ser	Ser	Leu	His	Val	Glu	Arg
210						215					220				
Trp	Ala	Phe	Asp	Val	Glu	Leu	Leu	Tyr	Ile	Ala	Gln	Phe	Phe	Lys	Ile
225					230					235				240	
Pro	Ile	Ala	Glu	Ile	Ala	Val	Asn	Trp	Thr	Glu	Ile	Glu	Gly	Ser	Lys
				245					250					255	
Leu	Val	Pro	Phe	Trp	Ser	Trp	Leu	Gln	Met	Gly	Lys	Asp	Leu	Leu	Phe
		260					265					270			
Ile	Arg	Leu	Arg	Tyr	Leu	Thr	Gly	Ala	Trp	Arg	Leu	Glu	Gln	Thr	Arg
		275				280						285			
Lys	Met	Asn													
	290														

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CNCCATCGGG GAACACCAGA AAGAACACT

29

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TNCTGCGCAT ATCCGTCAGG TTAAACTCC

29

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CNCTGGTTCT ACATCAATAC CAGCTTTCC

29

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TNACAACAGT GATATTTGAG AGCTTCAAG

29

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CNGTAACACC TCTCCAACGC TTTCGATGC

29

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GNCAAGGACA GACACGTGGA AATGAAGAC

29

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ANGTCCACCT CATAGTCATG GGCTCCTC

29

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TNTCAGCCAG CTCATGAAA ACAGGAAAC

29

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CNTGGGAAGC GGTAGCTGG AAGTCTGA

29

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TNTCTTCTTC ATGTCGATGG AGTGCTGGC

29

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 359 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Arg Val Lys Val Gln Leu Ala Leu Val Phe Phe Lys Asn Leu Ala Ser  
1 5 10 15

Ser Cys Thr Leu Asp Ser Ala Leu Asn Ala Ala Ser Tyr Tyr Asn Phe  
20 25 30

Thr Val Leu Lys Val Pro Arg Ser Met Thr Asp Pro Gln Asn Met Glu  
35 40 45

Phe Gln Val Pro Val Ile Leu Thr Ser Gln Ala Asn Ala Pro Leu Leu  
50 55 60

Ala Gly Asn Thr Cys Gln Asn Val Val Ser Gln Val Thr Tyr Glu Ile  
65 70 75 80

Glu Thr Asn Gly Thr Phe Gly Ile Gln Lys Val Ser Val Ser Leu Gly  
85 90 95

Gln Thr Asn Leu Thr Val Glu Pro Gly Ala Ser Leu Gln Gln His Phe  
 100 105 110  
 Ile Leu Arg Phe Arg Ala Phe Gln Gln Ser Thr Ala Ala Ser Leu Thr  
 115 120 125  
 Ser Pro Arg Ser Gly Asn Pro Gly Tyr Ile Val Gly Lys Pro Leu Leu  
 130 135 140  
 Ala Leu Thr Asp Asp Ile Ser Tyr Ser Met Thr Leu Leu Gln Ser Gln  
 145 150 155 160  
 Gly Asn Gly Ser Cys Ser Val Lys Arg His Glu Val Gln Phe Gly Val  
 165 170 175  
 Asn Ala Ile Ser Gly Cys Lys Leu Arg Leu Lys Lys Ala Asp Cys Ser  
 180 185 190  
 His Leu Gln Gln Glu Ile Tyr Gln Thr Leu His Gly Arg Pro Arg Pro  
 195 200 205  
 Glu Tyr Val Ala Ile Phe Gly Asn Ala Asp Pro Ala Gln Lys Gly Gly  
 210 215 220  
 Trp Thr Arg Ile Leu Asn Arg His Cys Ser Ile Ser Ala Ile Asn Cys  
 225 230 235 240  
 Thr Ser Cys Cys Leu Ile Pro Val Ser Leu Glu Ile Gln Val Leu Trp  
 245 250 255  
 Ala Tyr Val Gly Leu Leu Ser Asn Pro Gln Ala His Val Ser Gly Val  
 260 265 270  
 Arg Phe Leu Tyr Gln Cys Gln Ser Ile Gln Asp Ser Gln Gln Val Thr  
 275 280 285  
 Glu Val Ser Leu Thr Thr Leu Val Asn Phe Val Asp Ile Thr Gln Lys  
 290 295 300  
 Pro Gln Pro Pro Arg Gly Gln Pro Lys Met Asp Trp Lys Trp Pro Phe  
 305 310 315 320  
 Asp Phe Phe Pro Phe Lys Val Ala Phe Ser Arg Gly Val Phe Ser Gln  
 325 330 335  
 Lys Cys Ser Val Ser Pro Ile Leu Ile Leu Cys Leu Leu Glu Leu Gly  
 340 345 350  
 Val Leu Asn Leu Glu Thr Met  
 355

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2696 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGTGACCAT TCTTGCCAAC TTCTGGGCTG GCAGTATGGA GTCATCTCCC TATCTTTCAT	60
TGCGTGTGTG AAATCTACTT TCTGAATTCT GCCATTTCCT TCTTCACACT GTCTCTCTGGG	120
TTATCTTTGC TTCCTCACAT CCCTATCTCT CTTCCTATAA ACTGGCTCCC GTCACTTCCA	180
TGATCCCTTC AGTGGCTTCT GAGCTGGTCT CCTGACCCC AAAGCCTCAG CCTTCCAGTC	240
TCCCTACAAA ATCTCAGCAA GTTCATTTTA GGTAAAAATT TGGACATATT TTAATACGG	300
CTCACCACTT CATGTGAAAA TGATGGCACC CTACCAAGCA GTTTGCAGAG TTACGGTAAC	360
TGTTTCATGC TAATGATGTT ATTCATCCAG TTACAATTTT CTCAAAACCT CTTTGGGCAC	420
TCTTTATTTT TAATCAAAAT TTAAGCCAA TATTTCATTT TGAGAAATATG AATTAAATTG	480
GGAAATTCAT CCTGTGGTA CAGTTTACAG ATTTTAAATG TTTACCCATT TATCTGTGTT	540
TTTGATATAT TAATTTCCCA TATAGCTCCA GAGTTATGTG ATATTATTTT TTTGCCAGTA	600
TATTAGAAAA TGATTAATTT CTCATGACCA ACTTCTGAAA AGAAAGACCC AATGCAAAAT	660
GCAATCTATT ACAATTATTT TTTTGAATAA AAAAGAATAT ATTATAGTTC TTTAACATTT	720
GATATTTTAA ATTTGACATA TTCTTGATAT TTGTAAGAAA TTTCCACTGA ATGAATTTTA	780
CACAATTCAG ATACTACCAA TTAACATAAT CTAGCCTAAA CAAATAACAT TATTTTAAAA	840
TAACAAAATC TTTAAAAATA ATTTTCTATT TTGAACITTT AGCCATAATG TAAGAAAAATA	900
AAATTTTCTA GCAGAATAAT CAAAGAGTGA AACAAAGTTC CAACATGTTT TTTCTTTGCA	960
ATTAAACATG GCACTTTTAC AGTTATTTAT TATTCATATC AGTGCACCTA CCGACTTCAT	1020
ATTTTCAAAAT CAAAATACAG TGTTTTTCTC CAGTGAAATC CTTATTCTCA TGACTGATAG	1080
AAAACATTGC CAATTTTGAT ATTTCCAGAG TTAATGTAA ATTATTGAA AGAAAATTAT	1140
TTAAAAATAA AAAAATAGAC ATTTCAAGAC TATTTCTTAT CACATAATTC AAAAAGTACT	1200
TGGATCAAAAT CCTACAGAGT TTCTCCACTA AAATTCTACT TGTGCAGAGG GCATTGAAAC	1260
GCATGAAAAA CAACAGCAGC TTAGTTAGGT TAATTAATTC GGTAAATTAA GCACCTACTA	1320
CATGCTCAGC TCTATGCTAG GTGTCATGAG GAATTAAAAA GACATGTAAT GCACATTTTC	1380
TGATTTCAAG GAGCTTTAAA TATTATTGTG TAGAAAAAGT TAACATCTAT GAAAAATAGAA	1440
GTGGGGCAAT TTTGTGCTTA ATTCCATGGT CCAGATACAT CAAAAAATCA ATGTGGGCTG	1500

TCAAAGAAGG	TTTCTTGATA	GTCACTAGTC	AGCCTGATTC	TTGAAAGGAT	ATGTGGAATA	1560
TAAAAATTTTA	TTTATATTCC	TTTTGAGAAA	ATACTGAGAA	AACCATCTTC	CCTGAAAAAG	1620
AGAACGTATT	GTAAAGAAAG	TACATGAAAT	TGAAGGTGA	ATATCCAACA	TCCCCCACAC	1680
TGCCCCAGTG	TCTCTGCTCC	CTTACTGAGC	CTTACTATTA	TTCTTCATAG	CCCTATCACT	1740
ACCTAGTCTA	GTATTCACTG	AACTGTGTCA	TCCACTAGAA	TATGAGCATA	ATGAGAGCAG	1800
AGACTACACC	TGTCGGTTCA	GTATTCTATC	CTCAGCACAT	AGAATGGTAC	CTGGCACATA	1860
GCAGATGCTA	AAATAAAATT	TAAATGAATA	AATTAATTCA	ATCAACAAC	TCAAGGTGTT	1920
ATTATTACCT	ACAACATTAT	TTTACAAGAG	GTATGCACCG	TGGAAGATCC	TGGAGACACA	1980
ACAATGAATA	AAGCCAAGCC	AGTTCCCTGCC	CCCGTGAGC	TTGTAGTCAA	GACATTGAAC	2040
AAGTGATCAG	AAAGATGTTG	ACTGCTGCAG	CAGAGGGTTG	CAAGCTGCTC	ATGAGTATAT	2100
AACAAGTAGC	CCTAACCAAA	GCATTCTCTC	CCTTGGTTTA	ATGTCACCCC	ATTGAGGTGA	2160
CTGCTAAATA	CTAATCCATG	ACTCTATCCC	TTGGCATTCA	AACTCACACA	TCCACTTACC	2220
TGCTCTCCA	ACCTCATCTC	CCTCCACTCA	CAAGAGCCCA	TCATATTATT	CATCAAAATG	2280
AAACTGCACC	CAGTTCTTCT	GAACATATTA	CCTTACAAAA	CTTTCATTTA	TGCCTGGTGA	2340
CTCTCATCAG	GCATTCAAAA	GCTTCCCTC	AGTGCTTCAG	GGCTCTTCCT	TTTCTTCCCT	2400
TTATACATAC	ACCTTTATGT	ATCTTCATAC	GTACCCCTGA	TAACCTCATA	TATCTTAGCA	2460
TTTACCATAT	TCTGTTGAAA	AACTGTTTCC	ATTCTCTTT	ACTTACTAGA	ATGTAACAG	2520
ATGCACAATG	TTGAGAAAA	GAAAGTGAC	AACTTTGTTT	ACAAGTTTAG	AAATTATCAG	2580
ATTCTCACYT	AAGCTCTAGT	CTCTGTAAAG	TCCACAAC	CTYAATAAAA	GTGAAGAAAA	2640
ATGTTAAACG	AGAGGGAGGA	ATCAAAAACA	AAGAACTATT	TAAAAA	AAAAA	2690

(2) INFORMATION FOR SEQ ID NO:36:

## (ii) MOLECULE TYPE: protein

Met Thr Leu Ser Leu Gly Ile Gln Thr His Thr Ser Thr Tyr Leu Pro  
1 5 10 15

Leu Gln Pro His Leu Pro Pro Leu Thr Arg Ala His His Ile Ile His  
20 25 30

Gln	Asn	Glu	Thr	Ala	Pro	Ser	Ser	Ser	Glu	His	Ile	Thr	Leu	Gln	Asn
	35						40					45			
Phe	His	Leu	Cys	Leu	Val	Thr	Leu	Ile	Arg	His	Ser	Lys	Ala	Phe	Pro
	50					55					60				
Gln	Cys	Phe	Arg	Ala	Leu	Pro	Phe	Leu	Pro	Phe	Ile	His	Thr	Pro	Leu
65					70					75				80	
Cys	Ile	Phe	Ile	Arg	Thr	Leu	His	Asn	Leu	Ile	Tyr	Leu	Ser	Ile	Tyr
				85					90					95	
His	Ile	Leu	Leu	Lys	Asn	Cys	Phe	His	Phe	Ser	Leu	Leu	Thr	Arg	Met
				100				105						110	

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3614 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CGCGCTAACT GTGCTCTCCTCC GGGGCCCTCC GCCTGCTCCC AGCCATGGTG GCCTGGCGCT	60
CGCGCTTCTCT TGTCTGCCTC GCTTCTCTCT TGGCCACCCCT GGTCCAGCGA GGATCTGGGG	120
ACTTTGATGA TTTTAACCTG GAGGATGCAG TGAAGAAAC TTCTCTCAGTA AAGCGATCAC	180
TGTAAGGATG ACATGGGAGG AGCCATGTGA AGCACTCAGC ACGTCTCTTG GAACAAGAGC	240
CATGGGACCA CACCACCACC ACCACAACCA ATAGGCCAGG AACCACCAGA GCTCCGCGCA	300
AACCTCCAGG TAGTGGATTG GACTTGGCTG ATGCTTTGGA TGATCAAGAT GATGGCCGCA	360
GGAAACCGGG TATAGGAGGA AGAGAGAGAT GGAACCATGT AACCACCACG ACCAAGAGGC	420
CAGTAACCAC CAGAGCTCCA GCAAATACTT TAGGAAATGA TTTTGACTTG GCTGATGCC	480
TGGATGATCG AAATGATCGA GATGATGGCC GCAGGAAACC AATTGCTGGA GGAGGAGGTT	540
TTTCAGACAA GGATCTTGAA GACATAGTAG GGGGTGGAGA ATACAAACCT GACAAGGGTA	600
AAGGTGATGG CCGGTACGGC AGCAATGACG ACCCTGGATC TGGCATGGTG GCAGAGCCTG	660
GCACCATTGC CGGGGTGGCC AGCGCCCTGG CCATGGCCCT CATCGTGGCC GTCTCCAGCT	720
ACATCTCCTA CCAGCAGAAG AAGTTCTGCT TCAGCATTCA GCAGGCTCTC AACGCAGACT	780
ACGTGAAGGG AGAGAACCTG GAAGCCGTGG TATGTGAGGA ACCCAAGTG AAATACTCCA	840
CGTTGCACAC GCAGTCTGCA GAGCCGCCGC GCCTGCCCGC ACCAGCCCGG ATCTGAGGGC	900

CCTGTCCAGC TGCAGGCATG CACAATGGTG CCACCGCTTG TCACCCGGCT CCCCCACCC	960
CTTCATTTGG ACCCGCAGCT GCTGTGCTGC TCTGTGCCGT CGGCTCCTTG TTGGTCTGAG	1020
TTTCCCGGAT GAGCTCTGGG TGTTTGTGAG TTTGGTTTCT CTGCCCTGCC CCAAGCGTGC	1080
TGAGACTTGG TGCCGAAATT CAAGAGCCAG CTCTGATAGA AAGCCAGCAC CAGCCTCGGG	1140
AGCTGCTGAG CCACCAACTC CCAAGCCAG CCTGCCTCCA GCTTTACTGA GCACAGGATG	1200
CGGGGGCCAA GATGATGCTG AGGCCTGATG ACATTTATGC TTAGGGGACA AGAGTTTGAA	1260
CTCAAGGGAC TGTGACCCCT GCACACTGGA GTGGCTCATT GTGGCAGGTT TCTGCCAATA	1320
GACAGCCCTT GACAGTGCC TCAAGGAGCT GCAGGTGGG GGCTCAGCCT GCACCCACTT	1380
GGAGCCCCTG CAAGGAGCGA ACCGCTCAGC ACCAAGTAAC ACCACACACA CGCAGCACCC	1440
AGGATGATGG TTTCACTTCA GTCTTCCCCA TCCAGGTTT TATGTTGCTG GGCTTCCGGA	1500
GAGCCGGTCC AAGCGGAGGC TTTCAGTGAT TTAAGTACAA ACATGCATCT CGTGATAGTC	1560
CTGCCTTGAG AGCTTAGGAA TCTTCCGGAT AAGTATGAAG CAATTCGTAG GCCTGTTTCC	1620
CATCTGATTC CATAGGGGGC TGGGTGTGGC TTCGGGTTGA CATGAGAAAG GTCTTTAGCA	1680
ATCATTTCTG CACCGGAGAT GAGTTTATC CTGTGTTGGG GAGAGGTGCT CACCCCTCCAC	1740
CCTGTGTCCC TGTTTTGTA GCAAGAGTGA CCGATGTCAA GAACGAGCAT CAAAGCCAGA	1800
ATCTGCTTG TTTGCTTAA AATGTAATTG GGGCGGGCGG GGGAGGAGAG GGGAAAGAGA	1860
CATTGCTTG GTTTAGTGAA ACGCAGGTGA CTTTGTAGCT CTGTGCTCAG CCTACTTGTC	1920
TGCTCTGAGG GAGAGTGCGT GGGGAGCCAT GCTCACCCTG GCAAACACAG GAACCCCATG	1980
ACTCGCCCTT CACCTGGCGT GGAGCTGCCT GGTTTGGGCT GGAGCAGAGC TGGTTTCTCTG	2040
GAATGTTCTT TTGGCCACAC TATGGTTCTG TCCCGGTGAG CTCTGTTGTC AGAGGCTCAC	2100
GGGACAGAAC CACATGCTAG GGTCTAGGGC CCCTGTCTAC TGATAGTCAG TTTGCTGTGT	2160
CAGAAAGCAC TTCTGAAAGC AGATATGAGT CACCAGACAG GCAGGATCTT ACAAACCTCA	2220
CGGGCCTCTT TGGTCTGCAT GATGGCCCCA TGCCTTTCAT AGGCTGTCCA CTGAGCGGGA	2280
TTGTCTGCTG AGTGGGATGA GCCAACTCCA GTTCTTAAAG GAAACCACTG GAATCTGCAG	2340
CCCCACATG CATCTGTCTA ACGCATGCCT CGTGTTCTGTT TTGCAAACAT GCCTGTGGTG	2400
GAGGTGGTCT AGTTGTAGCC CTGTGCGTCT CAAGGCTGCC TTGTGAGGCC ATTCCACAGT	2460
CGTGCCCTTG AGCTCCTTAC CACCCCTTTT CCTGCTCGGC CCTTTAATCC CTGACAGACC	2520
TGGAAGTGTG GGCTGAAGGG GGACCTGCAG CACTGCAGAA ATGCCTCTGC GTGGTGCCAT	2580

GAAGGAAAGA AACCTTGGCC TGTCTCGAG AAGCTTCCCA TGCTTCAGGA AGTTAGTAAG 2640  
GGTGGGTGG CTTGCAGGAT TGGCCTGTTT CCAGGGCCTC CCACACTCAT TGGCCAGATT 2700  
GTGAACTTTG TCAGGCTTGT CCCTCCCTGA TACCAAGTAT GTCGAGAACC GATGGCCCCA 2760  
CCCTCTGGCT GGTGCTGGGC CGGAGGTGGC TATGGAGGAT TTTGGCATGC GTGGCCTGTC 2820  
GCCACCTGGA CAGCGTGACC TCAGGGGTG TCCACTTTAC CTTTATGGTG AGGCCTGTGCG 2880  
GATGGCTAAG TCCTTGA AAC CCTAGAGCTG TGACGTAGAA TATGTGCTGT CTGTGAGACC 2940  
GTGTTCCCA GAGCACTGAC TGCAGTTGAG AGAGACCCAT TTTGCTCTCC CTTACCGCCC 3000  
CCCCCCCCG TGCTTTCTG CACAAAGCCT AGAGCCTGGC ACTCAAGCCC ACCGGTGGCA 3060  
GCTCCTAGTG ACTGACATG CCTGGAAGAC CCCTCAGCCT TCTGTTTGCA GAACGTTTCA 3120  
TTCAGGAGCT TCTCCTTCCC ACAGACATCT TACACTTGCT CGACACTGCC ACCTGCAGAA 3180  
GCCTGGCGGG CTCTGGTCAC CATGTGTCTA TCTGAAGGTT GCACGTGCCA GCATGGGCCT 3240  
GTCCCAACGC AGAGGGGAGA CACAGTGGAC TGAAAGGACT GGTGAAAGT GGCCAATCTC 3300  
TGTCAGCTTA ATTTGGCAGA GAAAATTTGT AACAACTCTG AGCACATGCT GGGTGAAGTC 3360  
ACAGCTCAAG GAAAGATAAA GCTGGGCGGA AGGAGGTGTG CGTGGCTTCT GGGGTGGGAC 3420  
CCAGAGGGGA GGCTCTGGGA CAGGGGCTGG GGTTCAGTGC CAGGGCCCTG AGGAAGAAAT 3480  
GGGGACTGAT CTCAAAATTC CAGAATTCCC TGTACATCTG TTCACGTGCT TGTGTCCAGG 3540  
TGTGACTTGT AAACGTGCTA GTGTTTGCA TAAATAAAAT GGCACCGAGC AAAAAAAAAA 3600  
AAAAAAAAA AAAA 3614

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 229 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Val	Lys	His	Ser	Ala	Gln	Ser	Leu	Glu	Gln	Glu	Pro	Trp	Asp	His	Thr
1				5				10					15		
Thr	Thr	Thr	Thr	Thr	Asn	Arg	Pro	Gly	Thr	Thr	Arg	Ala	Pro	Ala	Lys
			20					25					30		
Pro	Pro	Gly	Ser	Gly	Leu	Asp	Leu	Ala	Ala	Asp	Ala	Leu	Asp	Asp	Gln
		35					40					45			

Asp Gly Arg Arg Lys Pro Gly Ile Gly Gly Arg Glu Arg Trp Asn His  
 50 55 60  
 Val Thr Thr Thr Thr Lys Arg Pro Val Thr Thr Arg Ala Pro Ala Asn  
 65 70 75 80  
 Thr Leu Gly Asn Asp Phe Asp Leu Ala Asp Ala Leu Asp Asp Arg Asn  
 85 90 95  
 Asp Arg Asp Asp Gly Arg Arg Lys Pro Ile Ala Gly Gly Gly Gly Phe  
 100 105 110  
 Ser Asp Lys Asp Leu Glu Asp Ile Val Gly Gly Gly Glu Tyr Lys Pro  
 115 120 125  
 Asp Lys Gly Lys Gly Asp Gly Arg Tyr Gly Ser Asn Asp Asp Pro Gly  
 130 135 140  
 Ser Gly Met Val Ala Glu Pro Gly Thr Ile Ala Gly Val Ala Ser Ala  
 145 150 155 160  
 Leu Ala Met Ala Leu Ile Gly Ala Val Ser Ser Tyr Ile Ser Tyr Gln  
 165 170 175  
 Gln Lys Lys Phe Cys Phe Ser Ile Gln Gln Gly Leu Asn Ala Asp Tyr  
 180 185 190  
 Val Lys Gly Glu Asn Leu Glu Ala Val Val Cys Glu Glu Pro Gln Val  
 195 200 205  
 Lys Tyr Ser Thr Leu His Thr Gln Ser Ala Glu Pro Pro Pro Pro Pro  
 210 215 220  
 Glu Pro Ala Arg Ile  
 225

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1077 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AATCGGGAGT CCACACAGCG TTAGGTTTTT TTTTGTGTTT GTTGTGTTGT TTTGTTTTTT	60
TCCAACCCCTC TTTCGGATGG ACGGGGGAAA GAGAGAAAGA AAAACGAGGG AAAATCAACA	120
AAATGTGCGA TGCAAAGAGT CGATTTTCGC GGGGTTTGTC AACTTCGCCA CTGCCGCAGC	180
CGAATCGACG TCGTCACGTG ACGGTCTGCC TCCGCCCTTA TTAACCTCA GCCCAGCGGC	240
GGTTTCCAGG ACCTCAGACT TTTTGCCGAG GCGGCAGTCC CTAGACGAAG CGAAGGAGGC	300



GGCGCCTGCC CCGCCACAA GAGCTGCCG CCGCGGTGT TATAGTCCA CCCCATCTGC	360
AAAGGAAGGG GGAGCGGAAA GAGCGGGATC TAGCGTGGGA TAAAGTGGG ACTACTACAG	420
TGTAAGTGGG CATGCGCCCC TCCTAGAAAT GATGGGAATG CAAAAGCCCT TGACTGCTCC	480
AGGACTCGAG GGATCCTCGG TGCCAGGATG CTGGGTCAAG CGCTCCGCCG GGACAGAGGA	540
CTCATACCAG GGAAATGGAG CCCAGCTCG TGATAAACTA CGACCCAAGC TGGGGGAGGA	600
ACCTAGTTTT CGAAAGGAAA ATAATATGCG CAAGCTTTAA CTGAGCAGTG GGATGGTCTT	660
AAATACCAA GGAATGACTT TAAATCTTGC TGGATGGGAC TGCCACTCAC CGCTAGAAAT	720
CGGGGATCAA CAGCAAATC TGGATGACCC TGTAACCACA TCTCCAGTTC AGCCCCGGCA	780
GGGCGATCCT CACCCACCAG CAAAGTACCA TCCACCTTAT TGATGACAGG GATCCGGGTC	840
TCCAGGTCCA CATCAAGGTG ATTAGGCTCT TCCATGCACT CCACCTCCAG CTGCAAACCC	900
AGAATCCACC CCCATGAGCA CATACTCTTC TTTGGGGGAG GGAGGGAGGG GGAGCAGGGC	960
CAATGGTAGT CATGAAATGA CTCTAGTAT TTCCATTCCC CCAGTCCCAC TGCCTTCATC	1020
AATTATTGGG AATAAAAAGA CAATCTAATC GTCAAAAAAA AAAAAAAAAA AAAAAA	1077

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 108 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met Asp Gly Gly Lys Arg Glu Arg Lys Thr Arg Glu Asn Gln Gln Asn	
1 5 10 15	
Val Arg Cys Lys Glu Ser Ile Phe Ala Gly Phe Val Asn Phe Ala Thr	
20 25 30	
Ala Ala Arg Glu Ser Thr Ser Ser Arg Asp Gly Leu Pro Pro Pro Leu	
35 40 45	
Leu Thr Leu Ser Pro Ala Ala Val Ser Arg Thr Ser Asp Phe Leu Pro	
50 55 60	
Arg Arg Gln Ser Leu Asp Glu Ala Lys Glu Ala Ala Pro Ala Pro Pro	
65 70 75 80	
Thr Arg Ala Ala Ala Arg Gly Cys Tyr Ser Ser Thr Pro Ser Ala Lys	
85 90 95	
Glu Gly Gly Ala Glu Arg Ala Gly Ser Ser Val Gly	

## (2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 588 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

TAAGAATTAA	AAATGTCATC	CAAACAAGAA	ATAATGAGTG	ACCAGCGGTT	TAGACGGGTT	60
GCAAAGGACC	CGAGATTTTG	GGAAATGCCA	GAAAAGGATC	GAAAAGTCAA	AATTGACACG	120
AGATTTCGAG	CCATGTTTCA	TGACAAGAAG	TTCAAGTTGA	ACTATGCCGT	GGATAAAAGA	180
GGGCGCCCCA	TTAGCCATAG	CACTACAGAG	GATTGGAAGC	GTTTTTACGA	CCTTTCAGAT	240
TCTGATTCCA	ATCTCTCTGG	TGAAGATAGC	AAAGCATTGA	GTCAAAAGAA	AATAAAGAAG	300
AAAAAAACCC	AGACTAAAAA	AGAAATCGAT	TCAAAAAATC	TAGTTGAGAA	AAAGAAAGAA	360
ACCAAGAAGG	CTAATCACAA	GGGTCTTGAA	AATAAACTG	ATTTAGATAA	TTCTATAGGA	420
ATTAAAAAAA	TGAAAACCTC	ATGTAAATTT	AAGATAGATT	CAACATAAG	TCCGAAGAAG	480
GATAGCAAAG	AATTTACACA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	540
AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA		588

## (2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 163 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met	Ser	Ser	Lys	Gln	Glu	Ile	Met	Ser	Asp	Gln	Arg	Phe	Arg	Arg	Val
1							5				10				15
Ala	Lys	Asp	pro	Arg	Phe	Trp	Glu	Met	Pro	Glu	Lys	Asp	Arg	Lys	Val
															30
Lys	Ile	Asp	Lys	Arg	Phe	Arg	Ala	Met	Phe	His	Asp	Lys	Lys	Phe	Lys
															45
Leu	Asn	Tyr	Ala	Val	Asp	Lys	Arg	Gly	Arg	Pro	Ile	Ser	His	Ser	Thr
															60
															50

Thr Glu Asp Leu Lys Arg Phe Tyr Asp Leu Ser Asp Ser Asp Ser Asn  
 65 70 75 80  
 Leu Ser Gly Glu Asp Ser Lys Ala Leu Ser Gln Lys Lys Ile Lys Lys  
 85 90 95  
 Lys Lys Thr Gln Thr Lys Lys Glu Ile Asp Ser Lys Asn Leu Val Glu  
 100 105 110  
 Lys Lys Lys Glu Thr Lys Lys Ala Asn His Lys Gly Ser Glu Asn Lys  
 115 120 125  
 Thr Asp Leu Asp Asn Ser Ile Gly Ile Lys Lys Met Lys Thr Ser Cys  
 130 135 140  
 Lys Phe Lys Ile Asp Ser Asn Ile Ser Pro Lys Lys Asp Ser Lys Glu  
 145 150 155 160  
 Phe Thr Gln

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2773 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GTATATTTTG GTTACTTAC TCCTCTATTT CAGAAATTGA AAAAGATCCC CAAGGATCTG	60
TTACTACTGC ATTTCCCTTCT TGCTCTGTCT ACAGCCTAGG CCAACTAGTC AGGGTCTGGA	120
CATGCATCTC CTAAGGAAG AACTGTGTAG CACCATTGAT CACAATGTAA CATTTCATG	180
CTGCATTAAG GGTGTCTCTC TCTAATCATG ATTGTACCTG TCTCTTCCTG GGTAAGGGA	240
GATTTTTTTT TTTTAATGTG TAAAGAAATTG ATGCSAGCCA GGAACATGTC TGTAGTCCCA	300
GCTACTTGGG CACACGCCCTG TAGTCCMSCG CCACTCGAGC ACACACCTGT AGTACCAGCT	360
ACTCTGGAGG CTGAGGCAGG AGGATCACTT GAGCCCAGGA GATTAAGACT GTAGTATACT	420
ATGATCGTGC CTGTGGCTAG CCACTGTGCT CCAGCCTGGG CAACACCATC GTAAAAATAA	480
ATAAATAAAT AAATAAATTG GGGAGGACAG CCTCACTGGT ATCAGACTTA CAGGACCAGA	540
TAGACAAGAT GGGTATAAGG GGAGCTGAAG TCTGTGTTCA TATGAGGAAG AGAAGACCAA	600
GCCCTGGGAC TTTGGCTGAA TTCTCCGTG GGGCTGGACG GCAGTGATCT CCTGTTCCCT	660
ATGTGTAAAC AAAGATTCCA GGGCGTGGTT TTGCACTCCT GTTGACTCT TTTAGAGGTG	720

GAAAAGAGGT GGATACTGAG ATCTAAGAGG AAAGGATAGT CATTACAGTT CTGAGATATG	780
CGCTCTCTCT ATTGTTCTCG WACACAAAGG GATAGTCTCT TTCTGAGAGC TGATGTCCTT	840
GCTTGGAGGT TAGCCCCAAA ACATGGCTCT TGTATTGTTC TAAGAGAAAA GGCTTTCATT	900
TTGGTTCTTC TGATTGGTGT TACCTACTGC CTAATATGTG TTCATTTTTT GACAGAGAGG	960
CAGACTATTG AAAAAGTCTG TGTGAACAGA GAGCAGTTCA TTAAGCCCAT TGCTTTCAGT	1020
AATGTGGCCT TGACCCCTTC TGCTTCCCCC TTCTCCCATG GAGCATGGCA GGGCTTGGTT	1080
ATTTAGAGTC CATACATGCA AGCCATTGAG AGACTTGTTT GCTCAAATGC AAGTTTGCTC	1140
AAAAACAGGT CCTGAAGGCT TGCTTAGGAT TACAGGGATG CTGGGTAAAG ACACCGTTCC	1200
TCTCTCTCGC TGGAGAAATC CCTGTTTCTC TGACTCCCTT TGTGATCCTC ACAGTAATGT	1260
ATTCTGTGCC ACTGTAGGAC ACAAGGCTCT GGGCCAGTAG AACAGGCAGA GAGGTGACAC	1320
TGGGCAGCAA GCTGAGAGCT CTTTCTAAAT GGAGTGAAGG AATTCAGTGG CCTAGTTTCG	1380
CCATTCTCTA ATGAGAAACC AAGGCCAGGC TGAAAAGTGC AATTAGATGT GGTGGATTGT	1440
GGTAACGGCC TCCAGATAAA GGGGTATACC CTGTGGAAGT GACTTTTCCC CAITTTGATCC	1500
CTTTTCAACT CTAAATGGCC AGGCCAGAG CAGAAGAAGG GTTGGGTCTG GAAGGAAGGC	1560
TCCAAAGGAT GAAAGCTTCT CCCTGATCAT AAGGAAGTGC ATCTTTATAG AATTGTTGTG	1620
CATAATGTCA GTAAATCCCT CTCAC TTGAC AAGGGACTGG ATTCACTTGG CCTTGAGACG	1680
GGCCAGTAGT TATCAGTGAG TCAAAGCAAA GTGAAAGTTT CAGGAGATGG GACCAATGCT	1740
GCAATGCTCG CCATAACAAA ATTCTTAAA AATAAAAAAG CTAATGTTAT AGCAACAAAA	1800
AAAGACTGAA GCAAAACCAC ACTGAAATGC ATCCCACTCC AGGAGAGGAA TTCTTAGCGT	1860
AACACTCTAA ATAAATGGAA GGAATCATCA CCTTCCCTAT TTTACCCTCG CCTTGTTCAC	1920
CAGGCTGCCC AGTGCTTACC ATGCAGAAAG CAGTCAGCTG TACTCTGGAA GTTTCTGTTC	1980
TTCTTTCCTG GGGCTTAGGA TATTCTGGGA GCTGTCTGAG CCTTGTGCTC AAGGCTTATC	2040
AGGTGATATA ATCTTCTCTG TCTGGGCTGC TTGCTGGAGG AATAGGAAGT GACATTATATA	2100
AGACACAGGC GGTGTGAGCA TCCATGTGTG GTCTTGGTCT AAACAGGCTC TTGAACAGGT	2160
TAAAGCAAC AGCAATAACA AAACAAAAAC TACTGATGCT GAGCGTTTGG ATCCTAGTAA	2220
TATTTCAAA ATTGTCTTC TGCATATGTT CTATCCATAT TTGATTTCAA TATACATTAT	2280
TAAGCTTTCT TGGGTACTAT TTTGCTGGG CTCTTGCCTG AAGGTGTGAC CTGTCTCATG	2340
ATCCTTAAAA GAGAGAGGCT TTTTTCATCC AAAGCTGTAG TGTGGGGAAC TGGGGTGGGA	2400
GAGGCACCTT TTGGAATTCT GAAAGAATCA TATCTGTGTA TATACATACT GAGTGGGGAA	2460

GGATGGGGGT TGGCAGGGGT TGAGGGAGGT GGGAACAAAC AGTGAGTATG GGAACAGGCA 2520  
 GTCACCTCGA GTGTGGGAGG TCACCTGGGT CCGTCGTCTT CCTTCTGTAT GGTGTGGGT 2580  
 TTATGTACAC ACTATAACAC TTCCTGTGTG AGTTCAATGA CCTGTCTGTG AGTGCTTTGG 2640  
 TGTATTGAGC CTCAGTACAC TCCAAGGGCA TTAAGTCAA GAACAGAAC CTGGAACAAA 2700  
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2760  
 AAAAAAAAAA AAA 2773

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Met Arg Ser Leu Tyr Cys Ser Arg Thr Gln Arg Asp Ser Leu Phe Ser  
 1 5 10 15  
 Gly Ala Asp Val Pro Ala Trp Arg Leu Ala Pro Lys His Gly Ser Cys  
 20 25 30  
 Ile Val Leu Arg Glu Lys Ala Phe Ile Leu Val Leu Ile Gly Val  
 35 40 45  
 Thr Tyr Cys Leu Ile Cys Val His Phe Leu Thr Glu Arg Gln Thr Ile  
 50 55 60  
 Glu Lys Val Cys Val Asn Arg Glu Gln Phe Ile Lys Pro Ile Ala Phe  
 65 70 75 80  
 Ser Asn Val Ala Leu Thr Pro Ser Ala Ser Pro Phe Ser His Gly Ala  
 85 90 95  
 Trp Gln Gly Leu Val Ile  
 100

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3119 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GGAAACATTA TGGATCTGTG GAGCTGCTTA TTCCAGTGA TGCTGATGGA GCCATCCAAA	60
GGGCTGGAAG ATTACAGAGTG GAAAATGGCT CTTACAGATGA GAATGCAACT GCCCTGCCTG	120
GTACTTGGCG AAGAACAGAC GTGCACTTAG AGAACCCAGA ATACCACACC AGATGGTATT	180
TCAATATTTT TTTAGGACAA GTCCATCAGA ACTACATTGG AAACGATGCC GAGAAGAGCC	240
CTTTCTTCTT GTCCGTGACC CTTTCTGACC AAAACAATCA ACGTGTCCCT CAATACCGTG	300
CAATTCTTTG GAGAAAAACA GGTACCCAGA AAATATGCCT TCCCTACAGT CCCACAAAAA	360
CTCTTCTGTG GAAGTCCATC TTAAGTGCCA TGAATCTGGA CAAATTGAG AAAGGCCCCA	420
GGGAAATTTT TCATCCTGAA ATACAAAAGG ACTTGCTGGT TCTTGAAGAA CAAGAGGGCT	480
CTGTGAATTT CAAGTTTGGG GTTCTTTTGG CCAAAGATGG GCAGCTCACT GATGATGAGA	540
TGTTACGCAA TGAATTTGGA AGCGAGCCTT TTCAAAAATT TTTAAATCTT CTGGGTGACA	600
CAATCACTCT AAAGGGCTGG ACGGGCTACC GTGGCGGTCT GGATACCAAA AATGATACCA	660
CAGGGATACA TTCAGTTTAT ACTGTGTACC AAGGGCATGA GATCATGTTT CATGTTTCCA	720
CCATGTTGCC ATATTCCAAA GAGAACAAAC AGCAGGTGGA AAGGAAACGC CACATTGGAA	780
ACGATATCGT CACCATTTGT TTCCAAGAAG GAGAGGAATC TTCTCTGACC TTTAAGCCTT	840
CCATGATCCG CTCCCACTTT ACACATATTT TTGCCTTAGT GAGATACAAT CAACAAAAATG	900
ACAATTACAG GCTGAAAATA TTTTCAGAAG AGAGCGTACC ACTCTTTGGC CCTCCCTTGC	960
CAACTCCACC AGTGTTTACA GACCACCAGG AATTACAGGA CTTTTTGCTA GTGAAATTAA	1020
TTAATGGTGA AAAAGCCACT TTGGAAACCC CAACATTGTC CCAGAAACGT CGGCGTACCC	1080
TGGATATGTT GATTAGATCT TTACACCAGG ATTTGATGCC AGATTGTCAT AAGAACATGC	1140
TTAATGACAG ATCTTTTAGT GATGTCTTAC CAGAGTCACC CAAGTCAGCG CGGAAGAAAG	1200
AGGAGGCCCC CCAGGCGGAG TTTGTTAGAA TAGGGCAGGC ACTAAAACCTG AAATCCATTG	1260
TGAGAGGGGA TGCTCCATCA AGCTTGGCAG CTTCAGGGAT CTGTAAAAAA GAGATGACCT	1320
TCCATCAGTG CCGGTGTTTG ACAGAACTCT GCCAGTGAAG CAAATGCATG TGCTTGAGAC	1380
CCTGGACCTT CTGGTTCTCA GAGCAGACAA AGGAAAAGAT GCTCGCCTCT TTGTCCTCAG	1440
GCTAAGTGCT CTGCAAAAGG GCCTTGAGGG GAAGCAGGCT GGAAGAGCA GGTCTGACTG	1500
CAGAGAAAAC AAGTTGGAGA AAACAAAAGG CTGCCACCTG TATGCTATTA ACACCTACCA	1560
CAGCAGAGAG CTGAGGATTG TGGTTGCAAT TCGGAATAAA CTGCTTCTGA TCACAAGAAA	1620
ACACAACAAG CCAAGCGGGG TCACCAGCAC CTCATTGTTA TCTCCCCTGT CTGAGTCACC	1680
TGTTGAAGAA TTCCAGTACA TCAGGGGAGAT CTGTCTGTCT GACTCTCCCA TGGTGATGAC	1740

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CTTAGTGGAT GGGCCAGCTG AAGAGAGTGA CAATCTCATC TGTGTGGCTT ATCGACACCA 1800
ATTTGATGTG GTGAATGAGA GCACAGGAGA AGCCTTCAGG CTGCACCACG TGGAGGCCAA 1860
CAGGGTTAAT TTTGTTGCAG CTATTGATGT GTACGAAGAT GGAGAAGCTG GTTTGCTGTT 1920
GTGTTACAAC TACAGTTGCA TCTATAAAAA GGTTTGCCCC TTTAATGGTG GCTCTTTTFT 1980
GGTTCAACCT TCTGCGTCAG ATTTCCAGTT CTGTTGGAAC CAGGCTCCCT ATGCAATTGT 2040
CTGTGCTTTC CCGTATCTCC TGGCCTTCAC CACCGACTCC ATGGAGATCC GCCTGGTGGT 2100
GAACGGGAAC CTGGTCCACA CTGCAGTCGT GCCGCAGCTG CAGCTGGTGG CCTCCAGGTC 2160
GGATATATAC TTCACAGCAA CTGCAGCTGT GAATGAGGTC TCATCTGGAG GCAGCTCCAA 2220
GGGGGCCAGT GCCCGAAAT CTCCTCAGAC ACCCCGGGGC CGAGATACTC CAGTATTTC 2280
TTCTTCCCTG GGGGAAGGTG AAATTCAATC AAAAACTCTG TACAAGATTC CACTTAGAAA 2340
CCTCGTGGGC AGAAGCATCG AACGACCTCT GAAGTCACCC TTAGTCTCCA AGGTATCAC 2400
CCCACCCACT CCCATCAGTG TGGGCCTTGC TGCCATTCCA GTCACGCACT CCTTGTCCCT 2460
GTCTCGCATG GAGATCAAAG AAATAGCAAG CAGGACCCGC AGGGAAC TAC TGGGCCTCTC 2520
GGATGAAGGT GGACCCAAAGT CAGAAGGAGC GCCAAAGGCC AAATCAAAC CCGGAAGCG 2580
GTTAGAAGAA AGCCAAGGAG GCCCCAAGCC AGGGGCAGTG AGGTATCTA GCAGTGACAG 2640
GATCCCATCA GGCTCCTTGG AAAGTGCTTC TACTTCCGAA GCCAACCCCTG AGGGGCACTC 2700
AGCCAGCTCT GACCAGGACC CTGTGGCAGA CAGAGAGGGC AGCCCGGTCT CCGGCAGCAG 2760
CCCCTTCCAG CTCACGGCTT TCTCCGATGA AGACATTATA GACTTGAAGT AACAGAGTTG 2820
AATCTCAITT GCCATCTTTA GTTTTCTTAT GGAGGTTTAT ACTCTTTAAA CAGTTCTGAT 2880
GTAATTTCTC AACAAAATGT GGCTTTTAGC CTGTCAAGTGA TCTATTGGAC CAAACCTTCT 2940
GCACACTCGG CCAGTTCCTT CTCCAATGTC CGGTGCCATC TTTCTTGACC TTGTTTCTT 3000
TCTGTTTCAAG AACCATCAGT CCCCTTGTA TAAAGGTGGT AGATTTCATT GAGGTTTATG 3060
ATTGAAACTT TGAATAAATC AAAAATACTC ATTCCTTAAAA AAAAAAAAAA AAAAAAAAAA 3119

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(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

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Met Asn Leu Asp Lys Phe Glu Lys Gly Pro Arg Glu Ile Phe His Pro
1      5      10      15

Glu Ile Gln Lys Asp Leu Leu Val Leu Glu Glu Gln Glu Gly Ser Val
20     25     30

Asn Phe Lys Phe Gly Val Leu Phe Ala Lys Asp Gly Gln Leu Thr Asp
35     40     45

Asp Glu Met Phe Ser Asn Glu Ile Gly Ser Glu Pro Phe Gln Lys Phe
50     55     60

Leu Asn Leu Leu Gly Asp Thr Ile Thr Leu Lys Gly Trp Thr Gly Tyr
65     70     75     80

Arg Gly Gly Leu Asp Thr Lys Asn Asp Thr Thr Gly Ile His Ser Val
85     90     95

Tyr Thr Val Tyr Gln Gly His Glu Ile Met Phe His Val Ser Thr Met
100    105    110

Leu Pro Tyr Ser Lys Glu Asn Lys Gln Gln Val Glu Arg Lys Arg His
115    120    125

Ile Gly Asn Asp Ile Val Thr Ile Val Phe Gln Glu Gly Glu Glu Ser
130    135    140

Ser Pro Ala Phe Lys Pro Ser Met Ile Arg Ser His Phe Thr His Ile
145    150    155    160

Phe Ala Leu Val Arg Tyr Asn Gln Gln Asn Asp Asn Tyr Arg Leu Lys
165    170    175

Ile Phe Ser Glu Glu Ser Val Pro Leu Phe Gly Pro Pro Leu Pro Thr
180    185    190

Pro Pro Val Phe Thr Asp His Gln Glu Phe Arg Asp Phe Leu Leu Val
195    200    205

Lys Leu Ile Asn Gly Glu Lys Ala Thr Leu Glu Thr Pro Thr Phe Ala
210    215    220

Gln Lys Arg Arg Arg Thr Leu Asp Met Leu Ile Arg Ser Leu His Gln
225    230    235    240

Asp Leu Met Pro Asp Leu His Lys Asn Met Leu Asn Arg Arg Ser Phe
245    250    255

Ser Asp Val Leu Pro Glu Ser Pro Lys Ser Ala Arg Lys Lys Glu Glu
260    265    270

Ala Arg Gln Ala Glu Phe Val Arg Ile Gly Gln Ala Leu Lys Leu Lys
275    280    285

Ser Ile Val Arg Gly Asp Ala Pro Ser Ser Leu Ala Ala Ser Gly Ile
290    295    300

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09746703.122100



Cys Lys Lys Glu Met Thr Phe His Gln Cys Pro Cys Leu Thr Glu Leu  
305 310 315 320

Cys Gln

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1592 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GACTTTTATA AAAAAGTCAA GCAGTACAAA AGGGTGTAAA GTGAAGTTAC TGTCCTTCCC	60
CTCCATAAAC CCCCTGACCT TGGGAAACTG TTGTTAACAG TTACTTGGGT AACTTTTCAG	120
ATATTTTGTG TGCATGTACA AATGTGAGTA TCTAATGTAA AAAAATCAAA CCAAGATAAA	180
GTGTAAACTG CTATGATGGA ATCCTGCCTT GTTCTGCTAT TAGTCTTCTG TTTAATAATC	240
AGCTTTTGTA TTAGGACAGT GGTAGGAAGA AGCCAGTATG TCCTGCAACA TAATTTGTGG	300
TTCTGGACTG GTCAGGATTT CCTGAATGCA GCCTTTATCT GGAAGCTCTG CCCTTCTCCA	360
TCTGGGATAC GCTTTTTCAT CCATCAAAAC TGTCACTCC CTCTGTGAAG CCTTCCTGA	420
CTATTCTCTG TCCCTCTTTC CTCTCTTCCC ACAAACACAA CTGTGTACGC GTGTCAACAA	480
AGAGTTAATC GTGCTTTTCT CTGTGCTACT TTTATACSTA GTATATGGTC CATTGTTTTG	540
CACCTTAATC ACTCTCTTGT AATGATTTGT TTACATGTCA GTCTCCAGC CAGACTGAGA	600
GCTCACCAGG GGCAGAAGCC GTGTTTTGTT TACTGCTGTA TTCTCGGTAC CTGGTACAAT	660
GCTTGGCATA CAGTTGGATG AACGGGAAAG TAATCTGAGC TGCCGGTGCT GTGGCAGTGC	720
AAAGTGGGCA TATTTGTGCC CTTGGACCAG ATGTAGCCCT TGATGCATT TGCAGGAACA	780
CGGCTTAGTT ATTGTTTACT TTGAAGCCCT TTTGCCTCTA CTCTCTCCCA TATATCTTCT	840
CCTGACAGGG TGAAGTCACC TATAGCATT CCTAGTGTAT GGAAGTATTA ATTTCTTTCT	900
TTACTGGAAG AGCTACTAGC TTTTCTTCAT ACAGTTTCCT CTGCTCCAGT TTCATAAGTT	960
TCTTTTGGC TTGTATCTGT TTAGGATCAG GTGATATGGC TTCATTCTCT ATGACTGAAG	1020
CCCGGCAACA TAACACTGAA ATTCGAATGG CAGTCAGCAA AGTGCGTGAT AAAATGGATC	1080
ATCTCATGAC TAAGGTTGAA GAGTTACAGA AACATAGTGC TGGCAATCC ATGCTTATTC	1140

CTAGCATGTC AGTTACAATG GAAACAAGCA TGATTATGAG CAACATCCAG CGAATCATTG 1200  
 AGGCCAAGGT GACAGAGGAG TTAGCAGCGG CCACTGCACA GKTCTCTCAT CTGCAGCTGA 1260  
 AAATGACTTG CTCACCAAAA AAAGGAAACA GAGCTGCAGA TGCAGCTGAC AGAAAGCCTG 1320  
 AAGGAGACAG ATCTTCTCAG GGGCCAGCTC ACCAAAGTGC AGGCAAAGCT CTCAGAGCTC 1380  
 CAAGAAACYT CTGAGCAAGC ACASTCCAAA TTCAAAAGTG AAAAGCAGAA CCGGAAACAA 1440  
 CTGGAACCTA AGGTGACATC CCTGGAGGAG GAACTGACTG ACCTTCGAGT TGAGAAGGAG 1500  
 TCCTTGGAAA AGGTAAGCTC TACAACCCAG TTTGCCAGAA TTAGCTGTTT AATAAACATT 1560  
 TTTATTTTCC TTTTACAAAA AAAAAAAAAA AA 1592

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Met	Glu	Val	Leu	Ile	Ser	Phe	Phe	Thr	Gly	Arg	Ala	Thr	Ser	Phe	Ser	1	5	10	15
Ser	Tyr	Ser	Phe	Leu	Cys	Ser	Ser	Phe	Ile	Ser	Phe	Phe	Leu	Ala	Cys	20	25	30	
Ile	Cys	Leu	Gly	Ser	Gly	Asp	Met	Ala	Ser	Phe	Leu	Met	Thr	Glu	Ala	35	40	45	
Arg	Gln	His	Asn	Thr	Glu	Ile	Arg	Met	Ala	Val	Ser	Lys	Val	Ala	Asp	50	55	60	
Lys	Met	Asp	His	Leu	Met	Thr	Lys	Val	Glu	Glu	Leu	Gln	Lys	His	Ser	65	70	75	80
Ala	Gly	Asn	Ser	Met	Leu	Ile	Pro	Ser	Met	Ser	Val	Thr	Met	Glu	Thr	85	90	95	
Ser	Met	Ile	Met	Ser	Asn	Ile	Gln	Arg	Ile	Ile	Gln	Ala	Lys	Val	Thr	100	105	110	
Glu	Glu	Leu	Ala	Ala	Ala	Thr	Ala	Gln	Xaa	Ser	His	Leu	Gln	Leu	Lys	115	120	125	
Met	Thr	Cys	Ser	Pro	Lys	Lys	Gly	Asn	Arg	Ala	Ala	Asp	Ala	Ala	Asp	130	135	140	
Arg	Lys	Pro	Glu	Gly	Asp	Arg	Ser	Ser	Gln	Gly	Pro	Ala	His	Gln	Ser	145	150	155	160

Ala Gly Lys Ala Leu Arg Ala Pro Arg Asn Xaa  
165 170

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1694 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GGGAAACGGG AAGCCGCTGC AAGTCCACCG CCTCAGCTAC CCAGATTGGG ATCTGCCACG	60
GCCCGCTTTA TGGACTAGTG TGGGCGGCAG GCTCCTTTCC GTCCCTGCCC TGCTGTACCC	120
CGCTCCTTGG AGACCCCTTG TATCCCTCCC GCAAGGTGGA ATCCGCAGGC TGGAGGCTCC	180
CAGGGGAGGC AAACGCCTGG CCTGCCCCGT CCCACGCGC CACCATGACC CTCCTGCTGC	240
TGCCCCCTTCT GCTGGCTCTCT CTGCTCGCGT CCTGCTCTG TAACAAAGCC AACAAGCACA	300
AGCCATGGAT TGAGGCAGAG TACCAGGGCA TCGTCATGGA GAATGACAAC ACGGTCCTAC	360
TGAATCCACC ACTCTTTGCC TTGGACAAGG ATGCCCCGCT GCGCTATGCA GGTGAGATCT	420
GCGGCTTCCG GCTCCATGGG TCTGGGGTGC CCTTTGAGGC TGTGATCCTT GACAAGGCGA	480
CAGGAGAGGG GCTGATCCGG GCCAAGGAGC CTGTGGACTG CGAGGCCAG AAGGAACACA	540
CCTTCACCAT CCAGGCCTAT GACTGTGGCG AGGGCCCCGA CGGGGCCAAC ACCAAGAAGT	600
CCCACAAGGC CACTGTGCAT GTGCGGGTCA ACGATGTGAA CGAGTTTGCC CCAAGTGTG	660
TGGAACGGCT GTATCGTGCG GCTGTGACAG AGGGGAAGCT GTACGATCGC ATCTGCGGG	720
TGGAAGCCAT TGACGGTGAC TGCTCCCCC AGTACAGCCA GATGCTGTAC TATGAGATTC	780
TCACACCCAA CACCCTTTC CTCATTGACA ATGACGGGAA CATTGAGAAC ACAGAGAAGC	840
TGCAGTACAG TGGTGAGAGG CTCTATAAGT TTACAGTGAC AGCTTATGAC TGTGGGAAGA	900
AGCGGGCAGC AGATGATGCT GAGGTGGAGA TTCAGGTGAA GCCCACCTGT AAACCCAGCT	960
GGCAAGGCTG GAACAAAAGG ATCGAATATG CACCAGGTGC TGGGAGCTTG GCTTTGTTC	1020
CTGGTATCCG CCTGAGAGACC TGTGATGAAC CACTCTGGAA CATTCAGGCC ACCATAGAGC	1080
TGCAGACCAG CCATGTGGCC AAGGGCTGTG ACCGTGACAA CTACTCAGAG CGGGCGCTGC	1140
GGAACACTCTG TGGTGTCTGCC ACTGGGAGG TGGATCTGTT GCCCATGCTT GGGCCCCAATG	1200
CCAACCTGGAC AGCAGGACTC TCGGTGCACT ACAGCCAGGA CAGCAGCCTG ATCTACTGTT	1260

TCAATGGCAC CCAGGCTGTG CAGGTGCCCC TGGGTGGCCC CAGTGGGCTG GGCTCTGGGC	1320
CCCAGGACAG CCTCAGTGAC CACTTCACCC TGTCCTTCTG GATGAAGCAT GGCCTAAGTC	1380
CCAACAAGGG CAAGAAGGAA GAGGAAACCA TCGTATGTAA CACTGTCCAG AATGGTGAGC	1440
CTCCCCCTCCA GGCAC TAGCC AGAGGGGGAA ACTGGCTTCT TGTCCTGCCT CTGTCACTGC	1500
CCAGTGTGTG ACTGTGAACA GGTCACTTCC CCTCTCTTCA TTTGTGAGGT GCAAGTGCCA	1560
GGTGTGATAT GCCTTGATTC TGTGCTTTAT CCCCAACATG ACATGTTGGA TCGTAAAAAA	1620
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	1680
AAAAAAAAAA AAAA	1694

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met Thr Leu Leu Leu Leu Pro Leu Leu Leu Ala Ser Leu Leu Ala Ser	
1 5 10 15	
Cys Ser Cys Asn Lys Ala Asn Lys His Lys Pro Trp Ile Glu Ala Glu	
20 25 30	
Tyr Gln Gly Ile Val Met Glu Asn Asp Asn Thr Val Leu Leu Asn Pro	
35 40 45	
Pro Leu Phe Ala Leu Asp Lys Asp Ala Pro Leu Arg Tyr Ala Gly Glu	
50 55 60	
Ile Cys Gly Phe Arg Leu His Gly Ser Gly Val Pro Phe Glu Ala Val	
65 70 75 80	
Ile Leu Asp Lys Ala Thr Gly Glu Gly Leu Ile Arg Ala Lys Glu Pro	
85 90 95	
Val Asp Cys Glu Ala Gln Lys Glu His Thr Phe Thr Ile Gln Ala Tyr	
100 105 110	
Asp Cys Gly Glu Gly Pro Asp Gly Ala Asn Thr Lys Lys Ser His Lys	
115 120 125	
Ala Thr Val His Val Arg Val Asn Asp Val Asn Glu Phe Ala Pro Val	
130 135 140	
Phe Val Glu Arg Leu Tyr Arg Ala Ala Val Thr Glu Gly Lys Leu Tyr	

145		150		155		160
Asp Arg Ile Leu	Arg Val Glu Ala	Ile Asp Gly Asp	Cys Ser Pro Gln			
	165		175			
Tyr Ser Gln Ile	Cys Tyr Tyr Glu	Ile Leu Thr Pro	Asn Thr Pro Phe			
	180		190			
Leu Ile Asp Asn	Asp Gly Asn Ile	Glu Asn Thr Glu	Lys Leu Gln Tyr			
	195		205			
Ser Gly Glu Arg	Leu Tyr Lys Phe	Thr Val Thr Ala	Tyr Asp Cys Gly			
	210		220			
Lys Lys Arg Ala	Ala Asp Asp Ala	Glu Val Glu Ile	Gln Val Lys Pro			
	225		235			240
Thr Cys Lys Pro	Ser Trp Gln Gly	Trp Asn Lys Arg	Ile Glu Tyr Ala			
	245		255			
Pro Gly Ala Gly	Ser Leu Ala Leu	Phe Pro Gly Ile	Arg Leu Glu Thr			
	260		270			
Cys Asp Glu Pro	Leu Trp Asn Ile	Gln Ala Thr Ile	Glu Leu Gln Thr			
	275		285			
Ser His Val Ala	Lys Gly Cys Asp	Arg Asp Asn Tyr	Ser Glu Arg Ala			
	290		300			
Leu Arg Lys Leu	Cys Gly Ala Ala	Thr Gly Glu Val	Asp Leu Leu Pro			
	305		315			320
Met Pro Gly Pro	Asn Ala Asn Trp	Thr Ala Gly Leu	Ser Val His Tyr			
	325		335			
Ser Gln Asp Ser	Ser Leu Ile Tyr	Trp Phe Asn Gly	Thr Gln Ala Val			
	340		350			
Gln Val Pro Leu	Gly Gly Pro Ser	Gly Leu Gly Ser	Gly Pro Gln Asp			
	355		365			
Ser Leu Ser Asp	His Phe Thr Leu	Ser Phe Trp Met	Lys His Gly Val			
	370		380			
Thr Pro Asn Lys	Gly Lys Lys Glu	Glu Glu Thr Ile	Val Cys Asn Thr			
	385		395			400
Val Gln Asn Gly	Glu Pro Pro Leu	Gln Ala Leu Ala	Arg Gly Gly Asn			
	405		415			
Trp Leu Leu Val	Pro Pro Leu Ser	Leu Pro Ser Val				
	420		425			

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1309 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CTGTCCTCCT	TTTGACAGAGG	TGGTGCAGG	CTCCTGTTTG	ACGGTATTAA	GAAACATCGA	60
GTCACCTTTG	CTGGACAGGA	GGAACCTTGG	GACATCCGGA	ACCTGCTCAT	CTGGATCAAG	120
AAGAATTTTG	TAAAGAGCG	GCCAGAGTTG	TTCATCCAGG	GAGACAGCGT	GCGGCCAGGA	180
ATTCTGGTGC	TGATTAACGA	TGCCGACTGG	GAGCTACTGG	GTGAGCTGGA	CTACCAGCTT	240
CAGGACCAGG	ACAGCGTCCT	CTTCATCTCC	ACTCTGCACG	GCGGCTGAGG	GCCCTTCTCT	300
GGGCCTGGGC	ACCCTTAGAG	GGGAGAACGA	AGCAATCAGA	CATCCCCCTG	GCCCTTGCTT	360
CCAGGTCTCC	CTGTCCCCCT	TGCCCTGCCTT	CTTCCCTGCT	CTGTCCCCTA	AGCTCCCTCC	420
AGGCAGGGAA	AAGAGGCCAG	GTGCTAAAAA	TGAGCCTTTC	TCAAGCACGT	GAGCAGCGGA	480
AGGCAGACAG	GCGCCAGAGC	CCAGCACTCC	CTTTTCCAGC	AGCTGTGGTG	GGGAGGGTT	540
CCCCTCCAGT	TTGTCAAGAG	TTGAAGGAGG	CTCTGTGGCC	AGGTGACCTG	GCTGCCTTCC	600
ACTCCTTGTA	CCTCAGTCTA	AACATGGAGT	GGCGCTGAC	AAGGCGCTCC	AGCCCCAGAG	660
CCAGCGTCTT	CATGGGGAAG	ATGAATGGAC	CTGAGTAGCT	GAAGGAAGGC	CCCTCCCTAC	720
CCAAAGACTG	GAGGCTTCTC	AGCCTCAATT	TCCCTGTCTG	TACAGCTGAG	GGCTCTGCCT	780
GTCCCCCACT	GCTATCAGTA	TGGAACCCCA	GCTGGGGTCC	CCTATTGAGT	GCCGACTCCC	840
CCCACCGCCA	GCAGCTGCTC	CTCCAGCCAC	ACCCTTCCCT	CTCCCCCAC	CCYTAGCCCT	900
TGACCCTGGC	TGGCTGCCCC	CGCTCCACAG	GCCACCAGAT	GGGCTCCTGA	GACCCTCCCC	960
AGGCTGCTTA	CAGCTCATTC	TGCTGGGGGT	AGAGATGAGG	GGAGGGAGTA	AGTTAAACCT	1020
TGGACTAGCA	AGTAGAAGCC	TGGGGGGATG	CGTGTGCCTC	AGTTTCTCTC	TCCACAACCTG	1080
AATATAGTGG	CTGAAAACCTG	GGGAGATACT	TGATGCGCG	AATGTCCGTT	TTCTCTCCCT	1140
TCCACCTCC	TGCAGGAAGC	AGGACGGGGC	AGGCAGCACC	TGTTAGGCAC	AGTGCTTTGC	1200
CCCTCCTCCC	CTTCCCTTCT	GGAAGTCTTG	GGGCCTCAGT	GCTTGCAACA	GCCGCGCTTG	1260
GGCAATAAAA	AGACTAGGTT	GTTTACTAAA	AAAAAAAAAA	AAAAAAAAAA		1309

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 amino acids  
(B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

```
Met Ala Arg Met Ser Val Phe Ser Pro Phe Pro Pro Pro Ala Gly Ser
 1           5           10           15

Arg Thr Gly Gln Ala Ala Pro Gly Arg His Ser Ala Leu Pro Leu Leu
 20           25           30

Pro Phe Pro Ser Gly Ser Leu Gly Ala Ser Val Leu Ala Thr Ala Gly
 35           40           45

Leu Gly Gln Ile Lys Asp
 50
```

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1740 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

```
GGCCCCGTGCG CTCATCAAC CAGCCAGCC TCATCTCTGC ACTCTCCCGG GACTATCGCA      60
ACCTGAAGCC CAGTGCTGTT GCCCCACAGA GAAAGATGCC ACTGGATGAC ACCAAACTGA      120
TTATCCACCA GAACTCAGC GTCTTAGAAG ATATTGTGGA GAATATCTCG GGGGAGTCCA      180
CCAAGTCTCG ACAGATTGCG TACCACTGCG TGCAGGAATC TGTTCAAGTC TCCCTGGCCC      240
TCTTTCCAGC TTTTATCCAT CAGTCAGATG TGAATGATGA GATGCTGAGC TTCTTCCTCA      300
CTCTGTTTCC AGGCCTTAGA GTACAGATGG GTGTGCCTTT CACTGAGCAA ATCATACAGA      360
CTTTCCTCAA CATGTTTACC AGAGAGCAGT TAGCCGAGAG CATCCTCCAC GAGGGCAGCA      420
CAGGCTGCCG GGTGGTGGAG AAGTTTCTGA AGATCTGCA GGTGGTGGTC CAGGAGCCAG      480
GCCAGGTGTT CAAGCCCTTC CTCCCAGCA TCATCGCCCT GTGATGGAG CAAGTGTATC      540
CCATCATTCG CGAGCGTCCC TCCCCTGATG TGAAGGCCGA GCTGTTTGA CTCCTTTTCC      600
GGACGCTCCA TCACAACTGG AGGTACTTCT TCAAGTCCAC CGTGTGGGCC AGTGTCAGCA      660
GGGGGATCGC TGAGGAGCAG ATGGAGAATG AGCCCCAGTT CAGTGCCATC ATGCAGGCTT      720
TCGGACAGTC CTTTCTCCAG CCCGACATCC ACCTTTTAA ACAAAATCTC TTCTACTTGG      780
```

AGACTCTCAA	CACCAAGCAG	AAGCTGTACC	ACAAGAAGAT	CTTCCGGA	GCCATGCTGT	840
TCCAGTTTGT	GAACGTGCTG	CTCCAGGTCC	TGGTCCACAA	GTCCCATGAT	CTTTCGCAGG	900
AGGAGATTGG	CATCGCCATC	TACAACATGG	CCTCAGTCGA	CTTTGATGGC	TTCTTTGCCG	960
CCTTCCTCCC	AGAGTTCTCT	ACCAGCTGTG	ATGGTGTGGA	TGCCAACCAG	AAAAGTGTGC	1020
TGGGGCGGAA	TTTCAAGATG	GATCGGGACC	TGCCCTCATT	CACCCAGAAT	GTGCACAGGC	1080
TGCTCAACGA	CCTGCGCTAC	TACAGACTCT	GCAACGACAG	CCTGCCCCCT	GGCACTGTGA	1140
AGCTCTAGGC	CTGTACTTGC	CTGGGGACAC	GGACTTCTGC	TGCTGCCACC	TGCGCCAGCC	1200
CTACCTTCCA	CCACAGATGT	CTCCAGATG	GGCCTTGGTC	ACACTCCTTG	GCTTCTCCCA	1260
CCGCAAGCAA	CGCTGCCTGC	CTCTGCCGCT	CCTCCACATC	TTGCCGCTGC	CCAGCAGAGC	1320
TGGCTTCTGG	GTCCACCTGA	GCACTGGACG	GTGCTCCCAG	GGCGTTGGAG	CAGGCGGAGG	1380
GGTGTGTGGC	CAGGTACTAG	GAGGCACCA	GAAATCCCCG	GGGTGGCCCC	ATGCAGACCA	1440
GGCGCACGTG	GTCATGGGG	CAGAAATGCC	AAGGACAGCT	CACGACAGTG	CMACCTTCTC	1500
ACCATTCCAG	CCAAGGAGAG	ATGTGACGTT	GGAAMTGYTY	TGGCMTTYT	GTCAAGCCTC	1560
CCCCGCCCAA	ATTGCCTTGA	RATYTYTGCT	CTTTGTGAGA	GATTTGCAAA	GACTCAMGTT	1620
TTTGTGTGTT	TTCATCATT	CCATTGTGAT	ACTAAGAAAC	TAAGAAGCTT	AATGAAAAGA	1680
AATAAAATGC	CTATGTTGTT	GTTCTAGGRR	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	1740

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Met	Pro	Leu	Asp	Asp	Thr	Lys	Leu	Ile	Ile	His	Gln	Thr	Leu	Ser	Val
1					5				10				15		
Leu	Glu	Asp	Ile	Val	Glu	Asn	Ile	Ser	Gly	Glu	Ser	Thr	Lys	Ser	Arg
			20					25					30		
Gln	Ile	Cys	Tyr	Gln	Ser	Leu	Gln	Glu	Ser	Val	Gln	Val	Ser	Leu	Ala
			35				40					45			
Leu	Phe	Pro	Ala	Phe	Ile	His	Gln	Ser	Asp	Val	Thr	Asp	Glu	Met	Leu
	50					55					60				



Ser	Phe	Phe	Leu	Thr	Leu	Phe	Arg	Gly	Leu	Arg	Val	Gln	Met	Gly	Val	65	70	75	80
Pro	Phe	Thr	Glu	Gln	Ile	Ile	Gln	Thr	Phe	Leu	Asn	Met	Phe	Thr	Arg	85	90	95	
Glu	Gln	Leu	Ala	Glu	Ser	Ile	Leu	His	Glu	Gly	Ser	Thr	Gly	Cys	Arg	100	105	110	
Val	Val	Glu	Lys	Phe	Leu	Lys	Ile	Leu	Gln	Val	Val	Val	Gln	Glu	Pro	115	120	125	
Gly	Gln	Val	Phe	Lys	Pro	Phe	Leu	Pro	Ser	Ile	Ile	Ala	Leu	Cys	Met	130	135	140	
Glu	Gln	Val	Tyr	Pro	Ile	Ile	Ala	Glu	Arg	Pro	Ser	Pro	Asp	Val	Lys	145	150	155	160
Ala	Glu	Leu	Phe	Glu	Leu	Leu	Phe	Arg	Thr	Leu	His	His	Asn	Trp	Arg	165	170	175	
Tyr	Phe	Phe	Lys	Ser	Thr	Val	Leu	Ala	Ser	Val	Gln	Arg	Gly	Ile	Ala	180	185	190	
Glu	Glu	Gln	Met	Glu	Asn	Glu	Pro	Gln	Phe	Ser	Ala	Ile	Met	Gln	Ala	195	200	205	
Phe	Gly	Gln	Ser	Phe	Leu	Gln	Pro	Asp	Ile	His	Leu	Phe	Lys	Gln	Asn	210	215	220	
Leu	Phe	Tyr	Leu	Glu	Thr	Leu	Asn	Thr	Lys	Gln	Lys	Leu	Tyr	His	Lys	225	230	235	240
Lys	Ile	Phe	Arg	Thr	Ala	Met	Leu	Phe	Gln	Phe	Val	Asn	Val	Leu	Leu	245	250	255	
Gln	Val	Leu	Val	His	Lys	Ser	His	Asp	Leu	Leu	Gln	Glu	Glu	Ile	Gly	260	265	270	
Ile	Ala	Ile	Tyr	Asn	Met	Ala	Ser	Val	Asp	Phe	Asp	Gly	Phe	Phe	Ala	275	280	285	
Ala	Phe	Leu	Pro	Glu	Phe	Leu	Thr	Ser	Cys	Asp	Gly	Val	Asp	Ala	Asn	290	295	300	
Gln	Lys	Ser	Val	Leu	Gly	Arg	Asn	Phe	Lys	Met	Asp	Arg	Asp	Leu	Pro	305	310	315	320
Ser	Phe	Thr	Gln	Asn	Val	His	Arg	Leu	Val	Asn	Asp	Leu	Arg	Tyr	Tyr	325	330	335	
Arg	Leu	Cys	Asn	Asp	Ser	Leu	Pro	Pro	Gly	Thr	Val	Lys	Leu	340	345	350			

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

ANTGTCCTTGA CTACAAGCTC CACGGGGGC

29

- (2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

TNGCCAAGGA GAAAGCGAGG CAGACAAGG

29

- (2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

ANATCGACTC TTTCATCGC ACATTTTGT

29

- (2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CNTTCTTCGG ACTTATGTTT GAATCTATC

29

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

CNTTCCTCTT AGATCTCAGT ATCCACCTC

29

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CNCAGACAGG GGAGATAACA ATGAGGTGC

29

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

TNCTATAGGT GACTTCACCC TGTCAGGAG

29

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

TNTTACAGGA GCAGGACGCG AGCAGAGAG

29

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

ANTCAGTTGT GGAGGAGGAA ACTGAGGCA

29

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

CNTCGAAACA GAGTGAGGAA GAAGCTCAG

29

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 262 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Met Val Ala Trp Arg Ser Ala Phe Leu Val Cys Leu Ala Phe Ser Leu  
1 5 10 15  
Ala Thr Leu Val Gln Arg Gly Ser Gly Asp Phe Asp Asp Phe Asn Leu  
20 25 30  
Glu Asp Ala Val Lys Glu Thr Ser Val Lys Gln Pro Trp Asp His  
35 40 45  
Thr Thr Thr Thr Thr Thr Asn Arg Pro Gly Thr Thr Arg Ala Pro Ala  
50 55 60  
Lys Pro Pro Gly Ser Gly Leu Asp Leu Ala Asp Ala Leu Asp Asp Gln  
65 70 75 80  
Asp Asp Gly Arg Arg Lys Pro Gly Ile Gly Gly Arg Glu Arg Trp Asn  
85 90 95  
His Val Thr Thr Thr Thr Lys Arg Pro Val Thr Thr Arg Ala Pro Ala  
100 105 110  
Asn Thr Leu Gly Asn Asp Phe Asp Leu Ala Asp Ala Leu Asp Asp Arg  
115 120 125  
Asn Asp Arg Asp Asp Gly Arg Arg Lys Pro Ile Ala Gly Gly Gly Gly  
130 135 140  
Phe Ser Asp Lys Asp Leu Glu Asp Ile Val Gly Gly Gly Glu Tyr Lys  
145 150 155 160  
Pro Asp Lys Gly Lys Gly Asp Gly Arg Tyr Gly Ser Asn Asp Asp Pro  
165 170 175  
Gly Ser Gly Met Val Ala Glu Pro Gly Thr Ile Ala Gly Val Ala Ser  
180 185 190  
Ala Leu Ala Met Ala Leu Ile Gly Ala Val Ser Ser Tyr Ile Ser Tyr  
195 200 205  
Gln Gln Lys Lys Phe Cys Phe Ser Ile Gln Gln Gly Leu Asn Ala Asp  
210 215 220

Tyr Val Lys Gly Glu Asn Leu Glu Ala Val Val Cys Glu Glu Pro Gln  
225 230 235 240

Val Lys Tyr Ser Thr Leu His Thr Gln Ser Ala Glu Pro Pro Pro Pro  
245 250 255

Pro Glu Pro Ala Arg Ile  
260

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Met His Val Leu Glu Thr Leu Asp Leu Leu Val Leu Arg Ala Asp Lys  
1 5 10 15  
Gly Lys Asp Ala Arg Leu Phe Val Phe Arg Leu Ser Ala Leu Gln Lys  
20 25 30  
Gly Leu Glu Gly Lys Gln Ala Gly Lys Ser Arg Ser Asp Cys Arg Glu  
35 40 45  
Asn Lys Leu Glu Lys Thr Lys Gly Cys His Leu Tyr Ala Ile Asn Thr  
50 55 60  
His His Ser Arg Glu Leu Arg Ile Val Val Ala Ile Arg Asn Lys Leu  
65 70 75 80  
Leu Leu Ile Thr Arg Lys His Asn Lys Pro Ser Gly Val Thr Ser Thr  
85 90 95  
Ser Leu Leu Ser Pro Leu Ser Glu Ser Pro Val Glu Glu Phe Gln Tyr  
100 105 110  
Ile Arg Glu Ile Cys Leu Ser Asp Ser Pro Met Val Met Thr Leu Val  
115 120 125  
Asp Gly Pro Ala Glu Glu Ser Asp Asn Leu Ile Cys Val Ala Tyr Arg  
130 135 140  
His Gln Phe Asp Val Val Asn Glu Ser Thr Gly Glu Ala Phe Arg Leu  
145 150 155 160  
His His Val Glu Ala Asn Arg Val Asn Phe Val Ala Ala Ile Asp Val  
165 170 175  
Tyr Glu Asp Gly Glu Ala Gly Leu Leu Leu Cys Tyr Asn Tyr Ser Cys  
180 185 190

Ile Tyr Lys Lys Val Cys Pro Phe Asn Gly Gly Ser Phe Leu Val Gln  
 195 200 205  
 Pro Ser Ala Ser Asp Phe Gln Phe Cys Trp Asn Gln Ala Pro Tyr Ala  
 210 215 220  
 Ile Val Cys Ala Phe Pro Tyr Leu Leu Ala Phe Thr Thr Asp Ser Met  
 225 230 235 240  
 Glu Ile Arg Leu Val Val Asn Gly Asn Leu Val His Thr Ala Val Val  
 245 250 255  
 Pro Gln Leu Gln Leu Val Ala Ser Arg Ser Asp Ile Tyr Phe Thr Ala  
 260 265 270  
 Thr Ala Ala Val Asn Glu Val Ser Ser Gly Gly Ser Ser Lys Gly Ala  
 275 280 285  
 Ser Ala Arg Asn Ser Pro Gln Thr Pro Pro Gly Arg Asp Thr Pro Val  
 290 295 300  
 Phe Pro Ser Ser Leu Gly Glu Gly Glu Ile Gln Ser Lys Asn Leu Tyr  
 305 310 315 320  
 Lys Ile Pro Leu Arg Asn Leu Val Gly Arg Ser Ile Glu Arg Pro Leu  
 325 330 335  
 Lys Ser Pro Leu Val Ser Lys Val Ile Thr Pro Pro Thr Pro Ile Ser  
 340 345 350  
 Val Gly Leu Ala Ala Ile Pro Val Thr His Ser Leu Ser Leu Ser Arg  
 355 360 365  
 Met Glu Ile Lys Glu Ile Ala Ser Arg Thr Arg Arg Glu Leu Leu Gly  
 370 375 380  
 Leu Ser Asp Glu Gly Gly Pro Lys Ser Glu Gly Ala Pro Lys Ala Lys  
 385 390 395 400  
 Ser Lys Pro Arg Lys Arg Leu Glu Glu Ser Gln Gly Gly Pro Lys Pro  
 405 410 415  
 Gly Ala Val Arg Ser Ser Ser Ser Asp Arg Ile Pro Ser Gly Ser Leu  
 420 425 430  
 Glu Ser Ala Ser Thr Ser Glu Ala Asn Pro Glu Gly His Ser Ala Ser  
 435 440 445  
 Ser Asp Gln Asp Pro Val Ala Asp Arg Glu Gly Ser Pro Val Ser Gly  
 450 455 460  
 Ser Ser Pro Phe Gln Leu Thr Ala Phe Ser Asp Glu Asp Ile Ile Asp  
 465 470 475 480  
 Leu Lys

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1748 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GTTTACTGAT ACGACACAAG ATCGGGAGAT TTTTGATCAC CATACTGAAG AGGATATAGA	60
TAAAGTGCT AACAGTGAT TGATAAAAAA CCTGAGCAGG ACCCCATCTA GTTGCAGCAG	120
CTCTCTGGAT TCAATCAAGG CTGATGGGAC CTCTCTGGAC TTCAGCACTT ACCGCAGTAG	180
TCAATGSGAA TCACAGTTTC TCAGAGATAC TATTTGTGAA GAGAGCTTGA GGGAGAAACT	240
CCAAGATGGG AGAATAACAA TAAGGGAGTT CTTTATACTT CTCCAGGTCC ACATCTTGAT	300
ACAGAAACCC CGACAGAGCA ATCTCCCAGG CAATTTTACT GTAAACACAC CACCTACTCC	360
AGAAGACCTG ATGTTAAGTC AATATGTTTA CCGACCCAAG ATACAGATTT ATAGAGAAGA	420
TTGTGAGGCT CGTCCCAAAA AGATTGAAGA ATTAAGGCTT TCTGCATCGA ACCAAGATAA	480
GCTGTGTGGT GATATAAATA AGAACCTGTG GGAATAAATG AGACACTGCT CTGACAAAGA	540
GCTGAAGGCC TTTGGAATTT ATCTTAACAA AATAAGTCA TGTTTACCA AGATGACTAA	600
AGTCTTCACT CACCAAGGAA AAGTGGCTCT GTATGGCAAG CTGGTGCACT CAGCTCAGAA	660
TGAGAGGGAG AAACCTCAAA TAAAGATAGA TGAGATGGAT AAAATACTTA AGAAGATCGA	720
TAAGTGCCTC ACTGAGATGG AAACAGAAAC TAAGAATTG GAGGATGAAG AGAAAAACAA	780
TCCTGTGGAA GAATGGGATT CTGAAATGAG AGCTGCAGAA AAAGAATTGG AACAGCTGAA	840
AACTGAAGAG GAGGAGCTTC AAAGAAATCT CTTAGAAGTG GAGGTACCAA AAGAGCAGAC	900
CCTTGCTCAA ATAGACTTTA TGCAAAAACA AAGAAATAGA ACTGAAGAGC TACTGGATCA	960
GTGAGCTTG TCTGAGTGGG ATGTCGTTGA GTGGAGTGAT GATCAAGCTG TATTCACCTT	1020
TGTTTATGAC ACGATACAAC TCACCATCAC CTTTGAAGAG TCAGTTGTTG GTTTCCTTT	1080
CCTGGACAAG CGTTATAGGA AGATTGTTGA TGTCAATTTT CAATCTCTGT TAGATGAGGA	1140
TCAAGCTCCT CCTTCCTCCC TTTTAGTTCA TAAGCTTATT TTCCAGTACG TTGAAGAAAA	1200
GGAATCCTGG AAGAAGACAT GTACAACCCA GCATCAGTTA CCCAAGATGC TTGAAGAATT	1260
CTCACTGGTA GTGCACCATT GCAGACTCCT TGGAGAGGAG ATTGAGTATT TAAAGAGATG	1320



GGGACCAAAT TATAACCTAA TGAACATAGA TATTAATAAT AATGAATTGA GACTTTTATT 1380  
 CTCCTAGCTCC GCAGCATTTG CAAAGTTTGA AATAACTTTG TTTCTCTCAG CCTATTATCC 1440  
 ATCTGTACCA TTACCTTCCA CCATTCCAGAA TCACGTTGGG AACACTAGCC AAGATGATAT 1500  
 TGCTACCATT CTATCTAAAG TGCCACTGGA GAACAACCTAC CTGAAGAATG TAGTCAAGCA 1560  
 AATTTACCAA GATCTGTTTC AGGACTGCCA TTTCTACCAC TAGACCCCTTG GACCACCATT 1620  
 GGAACAACCA AGCAGAATGT ACTTGATATT ATTTCAGGGT CCCATTGCTG TTCAGCCTTT 1680  
 GTTTTACGT CATTACAAGC TGAGTAAAT TCCTTCTGAT GATGTTATAA AAAAAAAAAA 1740  
 AAAAAAAA 1748

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Met Glu Ser Gln Phe Leu Arg Asp Thr Ile Cys Glu Glu Ser Leu Arg  
 1 5 10 15  
 Glu Lys Leu Gln Asp Gly Arg Ile Thr Ile Arg Glu Phe Phe Ile Leu  
 20 25 30  
 Leu Gln Val His Ile Leu Ile Gln Lys Pro Arg Gln Ser Asn Leu Pro  
 35 40 45  
 Gly Asn Phe Thr Val Asn Thr Pro Pro Thr Pro Glu Asp Leu Met Leu  
 50 55 60  
 Ser Gln Tyr Val Tyr Arg Pro Lys Ile Gln Ile Tyr Arg Glu Asp Cys  
 65 70 75 80  
 Glu Ala Arg Arg Gln Lys Ile Glu Glu Leu Lys Leu Ser Ala Ser Asn  
 85 90 95  
 Gln Asp Lys Leu Leu Val Asp Ile Asn Lys Asn Leu Trp Glu Lys Met  
 100 105 110  
 Arg His Cys Ser Asp Lys Glu Leu Lys Ala Phe Gly Ile Tyr Leu Asn  
 115 120 125  
 Lys Ile Lys Ser Cys Phe Thr Lys Met Thr Lys Val Phe Thr His Gln  
 130 135 140  
 Gly Lys Val Ala Leu Tyr Gly Lys Leu Val Gln Ser Ala Gln Asn Glu  
 145 150 155 160

Arg Glu Lys Leu Gln Ile Lys Ile Asp Glu Met Asp Lys Ile Leu Lys  
 165 170 175  
 Lys Ile Asp Asn Cys Leu Thr Glu Met Glu Thr Glu Thr Lys Asn Leu  
 180 185 190  
 Glu Asp Glu Glu Lys Asn Asn Pro Val Glu Glu Trp Asp Ser Glu Met  
 195 200 205  
 Arg Ala Ala Glu Lys Glu Leu Glu Gln Leu Lys Thr Glu Glu Glu Glu  
 210 215 220  
 Leu Gln Arg Asn Leu Leu Glu Leu Glu Val Pro Lys Glu Gln Thr Leu  
 225 230 235 240  
 Ala Gln Ile Asp Phe Met Gln Lys Gln Arg Asn Arg Thr Glu Glu Leu  
 245 250 255  
 Leu Asp Gln Leu Ser Leu Ser Glu Trp Asp Val Val Glu Trp Ser Asp  
 260 265 270  
 Asp Gln Ala Val Phe Thr Phe Val Tyr Asp Thr Ile Gln Leu Thr Ile  
 275 280 285  
 Thr Phe Glu Glu Ser Val Val Gly Phe Pro Phe Leu Asp Lys Arg Tyr  
 290 295 300  
 Arg Lys Ile Val Asp Val Asn Phe Gln Ser Leu Leu Asp Glu Asp Gln  
 305 310 315 320  
 Ala Pro Pro Ser Ser Leu Leu Val His Lys Leu Ile Phe Gln Tyr Val  
 325 330 335  
 Glu Glu Lys Glu Ser Trp Lys Lys Thr Cys Thr Thr Gln His Gln Leu  
 340 345 350  
 Pro Lys Met Leu Glu Glu Phe Ser Leu Val Val His His Cys Arg Leu  
 355 360 365  
 Leu Gly Glu Glu Ile Glu Tyr Leu Lys Arg Trp Gly Pro Asn Tyr Asn  
 370 375 380  
 Leu Met Asn Ile Asp Ile Asn Asn Asn Glu Leu Arg Leu Leu Phe Ser  
 385 390 395 400  
 Ser Ser Ala Ala Phe Ala Lys Phe Glu Ile Thr Leu Phe Leu Ser Ala  
 405 410 415  
 Tyr Tyr Pro Ser Val Pro Leu Pro Ser Thr Ile Gln Asn His Val Gly  
 420 425 430  
 Asn Thr Ser Gln Asp Asp Ile Ala Thr Ile Leu Ser Lys Val Pro Leu  
 435 440 445  
 Glu Asn Asn Tyr Leu Lys Asn Val Val Lys Gln Ile Tyr Gln Asp Leu  
 450 455 460

Phe Gln Asp Cys His Phe Tyr His  
465 470

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2298 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CTTTCTTTTG ATTGCTCTG CTTTAGCGTC TCTAAATCCG GTCACCATGT CGGACCCCGA	60
AGGCGAGACC TTGCGAAGCA CTTTCCCTC TTATATGGCC GAAGGCGAGC GGCTCTACCT	120
GTGCGGGGAA TTTTCTAAAG CCGCGCAGAG CTTCAGCAAC GCTCTTTACC TTCAGGATGG	180
AGACAAGAAC TGCGTGGTTG CTCGCTCAA GTGCTTCTG AAGATGGGAG ACTTGGAGAG	240
ATCCCTGAAG GATGCTGARG CTTGCTCCA GAGTGACCCA GCTTCTGTA AGGGGATTTT	300
GCAAAAGGCT GAGACACTGT ACACCATGGG AGACTTTGAG TTTGCCTTGG TATTCTATCA	360
TCGARGCTAC AAGCTGARGC CTGATCGGGA ATTCARARTT GGCATTGAGA AAGCCCAAGGA	420
AGCCATCAAC AACTCAGTGG GAAGTCCTTC TTCCATTAAG CTGGAGAACA AAGGGGACCT	480
CTCCTTCTTA AGCAAGCAGG CTGAGAATAT AAAAGCCCAG CAGAAGCCTC AGCCCATGAA	540
ACACCTCTTA CACCCACCA AGGGAGAGCC CAAGTGAAG GCCTCGCTCA AGAGTGAGAA	600
GACTGTCCGC CAGCTTCTGG GGGAGCTCTA CGTGGACAAA GAGTATTGG AGAAGCTCCT	660
ATTGGATGAA GACCTGATCA AAGGCACCAT GAAGGCGCGC CTGACTGTGG AGGACCTCAT	720
CATGACGGGC ATCAACTACC TGGATACTCA CAGCAACTTC TGGAGGCAGC AGAAGCCGAT	780
CTACGCCAGG GAGCGGGACC GGAAGCTGAT GCAAGAGAAA TGGCTGCGGG ACCACAAACG	840
CCGTCCCTCA CAGACAGCCC ATTACATCCT CAAGAGCCTG GAGGACATTG ATATGTTGCT	900
CACAAGTGGC AGTGCTGAAG GGAGTCTTCA GAAAGCTGAG AAAGTGCTGA AGAAGTACT	960
GGAATGGAAC AAGGAAGAGG TACCAACAA GGATGAACTG GTTGGAAACT TGTATAGCTG	1020
CATAGGGAAT GCCCAGATTG AGCTGGGGCA GATGGAGGCA GCCCTGCAGA GCCACAGAAA	1080
GGACYTGGAG ATCGCCAAGG AATATGACCT TCCTGATGCA AAATCGAGAG CCCTTGACAA	1140
CATTGCAGAA GTTTTGGCCA GAGTTGGGAA ATTCCAGCAA GCCATTGACA CGTGGGAAGA	1200
AAAGATCCCT CTGGCAAAAA CCACCTGGA GAAGACCTGG CTGTTCCACG AGATCGGCCG	1260

CTGCTACTTG GAGCTGGACC AGGCTTGCA GGCCTGCAAT TATGGCGAGA AGTCCCAGCA 1320  
 GTGTGCCGAG GAGGAAGGGG ACATTGAGTG GCAACTGAAT GCCAGTGTTT TGGTGGCCCA 1380  
 GGCAACAAGT AAGCTGAGAG ACTTCGAGTC AGCCGTGAAC AATTTTGAGA AGGCCCTGGA 1440  
 GAGAGCAAAG CTTGTGCATA ACAACGAGGC GCAGCAGGCC ATCATCAGTG CTTGGACGA 1500  
 TGCCAACAAG GGTATCATCA GAGAACTGAG GAAAACCAAC TACGTGGAGA ATCTCAAAGA 1560  
 AAAAAAGCAG GGAGAAGCTT CACTGTATGA AGATAGAATA ATAACAAGAG AGAAGGACAT 1620  
 GAGGAGAGTG AGAGATGAGC CCGAGAAGGT GGTGAAGCAG TGGGACCATA GTGAGGATGA 1680  
 GAAAGAGACA GATGAGGACG ATGAGGCTTT TGGGGAAGCT CTGCAGAGCC CAGCAAGCGG 1740  
 AAAGCAGAGT GTGGAAGCAG GAAAAGCCAG AAGCGATTGG GGAGCAGTTG CCAAGGGCCT 1800  
 GTCAGGAGAA TTAGGCACAA GATCAGGAGA AACAGGCAGG AAGCTACTAG AAGCTGGCAG 1860  
 AAGAGAGTCA AGAGAAATTT ATAGGAGGCC TTCGGGAGAA TTAGAGCAAA GACTCTCAGG 1920  
 AGAATTTCAGC AGACAGGAAC CAGAAGAACT AAAGAACTT TCAGAAGTGG GCAGAAGAGA 1980  
 SCCAGAAGAA YTGGAAGAAA CACAATTTGG AGAAATAGGA GAAACGAAAA AAACAGGAAA 2040  
 TGAGATGGAA AAGGAATATG AATGAAGCCA TCGGTAGAGA TGAGGATCAG GAAGCTGGTG 2100  
 TTCAGAGGGA TCATGGGATT TTATTAAGCT GGATTTTCAA GCGATTGTGC TGTATAGGA 2160  
 AAAATGAGGG TTTTACTTGT GCTGCTTTCC ATCACTATTT TGCCATTAAA TAGGTGTCTT 2220  
 TCCTCTTCTG MAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2280  
 AAAAAAAAAA AAAAAAAAAA 2298

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 672 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Met Ser Asp Pro Glu Gly Glu Thr Leu Arg Ser Thr Phe Pro Ser Tyr  
 1 5 10 15  
 Met Ala Glu Gly Glu Arg Leu Tyr Leu Cys Gly Glu Phe Ser Lys Ala  
 20 25 30  
 Ala Gln Ser Phe Ser Asn Ala Leu Tyr Leu Gln Asp Gly Asp Lys Asn  
 35 40 45  
 Cys Leu Val Ala Arg Ser Lys Cys Phe Leu Lys Met Gly Asp Leu Glu

50					55					60					
Arg	Ser	Leu	Lys	Asp	Ala	Glu	Ala	Ser	Leu	Gln	Ser	Asp	Pro	Ala	Phe
65					70					75					80
Cys	Lys	Gly	Ile	Leu	Gln	Lys	Ala	Glu	Thr	Leu	Tyr	Thr	Met	Gly	Asp
				85					90					95	
Phe	Glu	Phe	Ala	Leu	Val	Phe	Tyr	His	Arg	Xaa	Tyr	Lys	Leu	Xaa	Pro
			100					105					110		
Asp	Arg	Glu	Phe	Xaa	Xaa	Gly	Ile	Gln	Lys	Ala	Gln	Glu	Ala	Ile	Asn
		115					120					125			
Asn	Ser	Val	Gly	Ser	Pro	Ser	Ser	Ile	Lys	Leu	Glu	Asn	Lys	Gly	Asp
		130					135					140			
Leu	Ser	Phe	Leu	Ser	Lys	Gln	Ala	Glu	Asn	Ile	Lys	Ala	Gln	Gln	Lys
145					150					155					160
Pro	Gln	Pro	Met	Lys	His	Leu	Leu	His	Pro	Thr	Lys	Gly	Glu	Pro	Lys
				165					170					175	
Trp	Lys	Ala	Ser	Leu	Lys	Ser	Glu	Lys	Thr	Val	Arg	Gln	Leu	Leu	Gly
			180					185					190		
Glu	Leu	Tyr	Val	Asp	Lys	Glu	Tyr	Leu	Glu	Lys	Leu	Leu	Leu	Asp	Glu
		195					200					205			
Asp	Leu	Ile	Lys	Gly	Thr	Met	Lys	Gly	Gly	Leu	Thr	Val	Glu	Asp	Leu
		210					215					220			
Ile	Met	Thr	Gly	Ile	Asn	Tyr	Leu	Asp	Thr	His	Ser	Asn	Phe	Trp	Arg
225					230					235					240
Gln	Gln	Lys	Pro	Ile	Tyr	Ala	Arg	Glu	Arg	Asp	Arg	Lys	Leu	Met	Gln
			245					250					255		
Glu	Lys	Trp	Leu	Arg	Asp	His	Lys	Arg	Arg	Pro	Ser	Gln	Thr	Ala	His
			260					265					270		
Tyr	Ile	Leu	Lys	Ser	Leu	Glu	Asp	Ile	Asp	Met	Leu	Leu	Thr	Ser	Gly
		275					280					285			
Ser	Ala	Glu	Gly	Ser	Leu	Gln	Lys	Ala	Glu	Lys	Val	Leu	Lys	Lys	Val
		290					295					300			
Leu	Glu	Trp	Asn	Lys	Glu	Glu	Val	Pro	Asn	Lys	Asp	Glu	Leu	Val	Gly
305				310					315					320	
Asn	Leu	Tyr	Ser	Cys	Ile	Gly	Asn	Ala	Gln	Ile	Glu	Leu	Gly	Gln	Met
			325						330					335	
Glu	Ala	Ala	Leu	Gln	Ser	His	Arg	Lys	Asp	Leu	Glu	Ile	Ala	Lys	Glu
			340					345					350		
Tyr	Asp	Leu	Pro	Asp	Ala	Lys	Ser	Arg	Ala	Leu	Asp	Asn	Ile	Gly	Arg
		355					360						365		

Val	Phe	Ala	Arg	Val	Gly	Lys	Phe	Gln	Gln	Ala	Ile	Asp	Thr	Trp	Glu	
370						375					380					
Glu	Lys	Ile	Pro	Leu	Ala	Lys	Thr	Thr	Leu	Glu	Lys	Thr	Trp	Leu	Phe	
385					390					395					400	
His	Glu	Ile	Gly	Arg	Cys	Tyr	Leu	Glu	Leu	Asp	Gln	Ala	Trp	Gln	Ala	
				405					410					415		
Gln	Asn	Tyr	Gly	Glu	Lys	Ser	Gln	Gln	Cys	Ala	Glu	Glu	Glu	Gly	Asp	
			420					425					430			
Ile	Glu	Trp	Gln	Leu	Asn	Ala	Ser	Val	Leu	Val	Ala	Gln	Ala	Gln	Val	
		435					440					445				
Lys	Leu	Arg	Asp	Phe	Glu	Ser	Ala	Val	Asn	Asn	Phe	Glu	Lys	Ala	Leu	
	450					455					460					
Glu	Arg	Ala	Lys	Leu	Val	His	Asn	Asn	Glu	Ala	Gln	Gln	Ala	Ile	Ile	
465				470					475						480	
Ser	Ala	Leu	Asp	Asp	Ala	Asn	Lys	Gly	Ile	Ile	Arg	Glu	Leu	Arg	Lys	
			485						490					495		
Thr	Asn	Tyr	Val	Glu	Asn	Leu	Lys	Glu	Lys	Ser	Glu	Gly	Glu	Ala	Ser	
			500					505					510			
Leu	Tyr	Glu	Asp	Arg	Ile	Ile	Thr	Arg	Glu	Lys	Asp	Met	Arg	Arg	Val	
		515					520					525				
Arg	Asp	Glu	Pro	Glu	Lys	Val	Val	Lys	Gln	Trp	Asp	His	Ser	Glu	Asp	
	530					535					540					
Glu	Lys	Glu	Thr	Asp	Glu	Asp	Asp	Glu	Ala	Phe	Gly	Glu	Ala	Leu	Gln	
545					550					555					560	
Ser	Pro	Ala	Ser	Gly	Lys	Gln	Ser	Val	Glu	Ala	Gly	Lys	Ala	Arg	Ser	
				565					570					575		
Asp	Leu	Gly	Ala	Val	Ala	Lys	Gly	Leu	Ser	Gly	Glu	Leu	Gly	Thr	Arg	
		580						585					590			
Ser	Gly	Glu	Thr	Gly	Arg	Lys	Leu	Leu	Glu	Ala	Gly	Arg	Arg	Glu	Ser	
	595					600						605				
Arg	Glu	Ile	Tyr	Arg	Arg	Pro	Ser	Gly	Glu	Leu	Glu	Gln	Arg	Leu	Ser	
	610					615					620					
Gly	Glu	Phe	Ser	Arg	Gln	Glu	Pro	Glu	Glu	Leu	Lys	Lys	Leu	Ser	Glu	
625					630					635				640		
Val	Gly	Arg	Arg	Xaa	Pro	Glu	Glu	Leu	Gly	Lys	Thr	Gln	Phe	Gly	Glu	
				645					650					655		
Ile	Gly	Glu	Thr	Lys	Lys	Thr	Gly	Asn	Glu	Met	Glu	Lys	Glu	Tyr	Glu	
		660						665					670			

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1010 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

GGAAGAGCCA CCATCCCTGC CCCCGTTTTT CCACCGGGGA GTCTGTACAG AGATTTTCT 60  
ACGTTTTTAT TTTTGCCTC AGAGGGATGG GATTGGGGAG GAGGGGATGG GCAGCGGAGG 120  
GTTGGGGGCA TGGTCTGCAG GCTCATCTGT GTCCGCCTTT CACTCCACTA ATGCTGTCTC 180  
AGTGTTTTCT CTCCTCTCTT TCGAGCTTG CACTCCGGTA CCCGACCCGG CGCCCTGGCC 240  
CATCCCATGC CGGGGGGCCA GTGGAAAGAA GACAGGCCGT CCAGCCCGTG CCCGCCTGCG 300  
GCGGGGGCAC CCAGCAAGCC CGCCCACCGC CCGTGCCTC ACCTGCTTCG CCACAGACTC 360  
TTGTTCCCGC CCCCTTGGGG CCTCCGTGTT TGGGGTGGGG GAGCTGCTTA GAGACTGTGC 420  
CCGTCCCTCG CCCCCACCC TGAAGTGCCA GCACCACCAG CACCAGATCT TCCGCCGCCA 480  
CACCGCATTG AGGACACGCG GGCCGGGCCG CTTCTGTCTA AGTTGTATAA AGTTGTCTCC 540  
GTGTCCCTCT CTCCTCTGCG CCCAGTGTT TCTTCTGATT TTTTTTCCC CTTTCCCTCC 600  
CTCCCTCTCC GCATTCTTCC CTTGGTTCAG CACAGGTAAA ACGGTTCCCC TCCCTCCCTG 660  
CCTTCATGGA TCACCAGCTC ACGTCATGTT GCCTTCTCTT TTCTTGTGT GTGTGTTTAT 720  
TTAAGTTATT TTTCTTCTC CTCTCCCTTT TCTTTTGGC CTTCCCTCCC TCCCTCTTCT 780  
GCCATGTAAC TGGAGGATGT GCTATGAGTT TGCAAACAGC TGAGCTGTCA GGCTGCTTTT 840  
TTTTCAGAT GTTCTTCTC TGCTTCCCTT TCCCTCCTC TCCCTCCTT TTCCTCTCTT 900  
CCTTCTTTC CTTGGAGCAC TGAGCACCAT TTGGAAGCTT GAGAGAAACC AAAATTAAAG 960  
AGAGAAAGAG AGAGCGTGCA CGCTCCTGCT TTGTCAAAAA AAAAAAAAAA 1010

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 205 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Met Gly Ser Gly Gly Leu Gly Ala Trp Ser Ala Gly Ser Ser Val Ser  
1 5 10 15  
Ala Phe His Ser Thr Asn Ala Val Ser Val Phe Ser Leu Ser Leu Phe  
20 25 30  
Arg Ala Cys Thr Pro Val Pro Asp Pro Ala Pro Trp Pro Ile Pro Cys  
35 40 45  
Arg Gly Ala Ser Gly Lys Lys Thr Gly Arg Pro Ala Arg Ala Arg Leu  
50 55 60  
Arg Arg Gly His Pro Ala Ser Pro Pro Thr Ala Arg Cys Leu Thr Cys  
65 70 75 80  
Phe Ala Thr Asp Ser Cys Ser Gln Pro Leu Gly Ala Ser Val Phe Gly  
85 90 95  
Val Gly Glu Leu Leu Arg Asp Cys Ala Arg Pro Arg Pro Thr Leu  
100 105 110  
Lys Cys Gln His His Gln His Gln Ile Phe Arg Arg His Thr Ala Leu  
115 120 125  
Arg Thr Arg Arg Pro Gly Arg Phe Val Ser Ser Cys Ile Lys Leu Ser  
130 135 140  
Pro Cys Pro Leu Leu Pro Leu Pro Val Phe Leu Leu Ile Phe Phe  
145 150 155 160  
Ser Pro Phe Pro Pro Ser Leu Ser Ala Phe Phe Pro Trp Phe Ser Thr  
165 170 175  
Gly Lys Thr Val Pro Leu Pro Pro Cys Leu His Gly Ser Pro Ala His  
180 185 190  
Val Met Leu Pro Ser Leu Phe Phe Val Cys Val Phe Ile  
195 200 205

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2409 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

ATTTYGCTCA TCAACCTCAT TATAGAACAT ATGATTGTG ATACAGATCC TGAACCTGGA 60  
GGAGCAGTCC AGCTTATGGG CCTGCTCGA ACTTTAGTTG ACCCAGAGAA CATGCTAGCC 120  
ACTGCCMATA AAACASAAAA GACTGAATTT CTGGGTTTCT TCTACAAGCA CTGTATGCAT 180



GTTCTCWCTG CTCCTTTACT AGCAAATACA ACAGAAGACA AACCTAGTAA AGATGATTTT	240
CAGACTGCCC AACTATTGGC ACTTGTATTG GAATTGTTAA CATTTTGTGT GGAGCACCAT	300
ACCTACCACA TAAAGAACTA CATTATTAAT AAGGATATCC TCCGAGAGT GCTAGTTCTT	360
ATGGCCTCGA AGCATGCTTT CTTGGCATTG TGTGCCCTTC GTTTTAAAG AAAGATTATT	420
GGATTAAAG ATGAGTTTGA CAACCGCTAC ATAATGAAA GTTTTTGTG TGAACCACTA	480
GTGAAGCAT TTCTCAACAA TGGATCCCGC TACAATCTGA TGAACCTGCG CATAATAGAG	540
ATGTTTGAAT TTATTAGAGT GGAAGATATA AAATCATTAA CTGCTCATGT AATTGAAAAT	600
TACTGGAAAG CACTGGAAGA TGTAGATTAT GTACAGACAT TTAAAGGATT AAAACTGAGA	660
TTTGAAACAC AAAGAGAAAG GCAAGATAAT CCCAAACTTG ACAGTATGCG TTCCATTTTG	720
AGGAATCACA GATATCGAAG AGATGCCAGA ACACTAGAAG ATGAAGAAGA GATGTGGTTT	780
AACACAGATG AAGATGACAT GGAAGATGGA GAAGCTGTAG TGCTCCATC TGACAAAAC	840
AAAAATGATG ATGATATTAT GGATCCAATA AGTAAATTCA TGGAAAGGAA GAAATTAAAA	900
GAAAGTGAGG AAAAGGAAGT GCTTCTGAAA ACAAACTTT CTGGACGGCA GAGCCCAAGT	960
TTCAAGCTTT CCCTGTCCAG TGGAAACGAAG ACTAACCTCA CCAGCCAGTC ATCTACAACA	1020
AATCTGCTG GTTCTCCGGG ATCACCTGGA TCCCCAGGAT CTCCAGGCTC TCCTGGATCC	1080
GTACCTAAAA ATACATCTCA GACGGCAGCT ATTACTACAA AGGGAGGCTC CGTGGSTCTG	1140
GTAGATTATC CTGATGATGA TGAAGATGAT GATGAGGATG AAGATAAGGA AGATACGTTA	1200
CCATTGTCAA AGAAAGCAAA ATTTGATTCA TAATAATGGC AACGGCCTAG GATCAGTACC	1260
TGTTGAAAAA AACTGGTTCT CCACCCCTCC CCCATACAAA ATCCACAAAA AAGCGCAGTG	1320
GTCTCTTGTS AATGACTGAC ACAGATCAGC CTCTTACACT TGACTTCTGC TCATCAAGTG	1380
CCAATTCAAT GGAGCAGGAG GAGGGGATAT CATATATTTA GGGGAAAGAC TTAAGCCTTT	1440
GAGCTCTCCA GCTTGGACCA CACATTGCCC TTTTCTCAGG GAAGGAAATG GAAACAAAAA	1500
GCCAACAGGG CAGGGGTTTT GTAAGTGGAA CTCGAGGATG ACTGGTCAGT TGCTACAATC	1560
AGAATATGCT TTCTTGGAAC ATGTTTGAGA CTCAGAAGAA TGGCCTTTCT GCCATAATTC	1620
TTCACTAGTC AAGAATGCCA GCAGTTTCTT TGTATAAAGA GACCTGCCTT TAAATCATA	1680
CATTCTGAAC ATTTIAGTCA AGCTACAACA GGTTTGAAA ACCTCTGTGG GGGAGGGGCG	1740
AGTATAAAGT TTCTCTCTT TTTAACTGTT CCCTTTGCC TCAAACTGC AGATATTTTT	1800
TTTTTTAAGT GGGGACTTCT CCCTACTTGA TTAAGATTG AGTGAATTC TAGATGTGST	1860

CATTGTGTC ATAATTTTT TGTTTTATTT TGTTTTGAT TTTTTTTTC CTCCTGAG 1920  
 TGTATGCTTA GTTGTGAGT ATATATATTT GGGACCATTA AACTTTTTT TGATGTAATA 1980  
 TAACCTAACG TTGTGCTGGT ACCTGTTTIA CCATGTGTAA TTTTGTCTT ACATCACAGT 2040  
 TCTTAATTG TTTAGAGTTT TATGAAAGAT GGTATAGTTT TTATTGACAA AAGCAAAGTA 2100  
 ATCTTACAAC TATGTGCATA CAAAAGCAAT ACTATTTTGT GACTAAATAT TTTATATTAA 2160  
 AATTACATC AGCAACTGTC TTGAGAAATC AGGGAATAG AATGGAATTT AAAACTTCAA 2220  
 CAGTTTGTGT AAATCTAGAA ACATGAAATT RGTATCCAA AGAGATTCTG AAATTTCTTT 2280  
 TCTKGGGGAA ATGACGGTAC ATTAATCAAA AATTGREGGAT GGATGATTTA AAAACATTG 2340  
 ACTTTTTAAT AATAAAAAGA AAAGTGAAGA GTAAGAGAAA TTGTAAGAAA AAAAAAAAAA 2400  
 AAAAAAAAAA 2409

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Met	Ile	Cys	Asp	Thr	Asp	Pro	Glu	Leu	Gly	Gly	Ala	Val	Gln	Leu	Met
1				5				10					15		
Gly	Leu	Leu	Arg	Thr	Leu	Val	Asp	Pro	Glu	Asn	Met	Leu	Ala	Thr	Ala
			20				25					30			
Xaa	Lys	Thr	Xaa	Lys	Thr	Glu	Phe	Leu	Gly	Phe	Phe	Tyr	Lys	His	Cys
		35				40						45			
Met	His	Val	Leu	Xaa	Ala	Pro	Leu	Leu	Ala	Asn	Thr	Thr	Glu	Asp	Lys
		50			55					60					
Pro	Ser	Lys	Asp	Asp	Phe	Gln	Thr	Ala	Gln	Leu	Leu	Ala	Leu	Val	Leu
65			70						75					80	
Glu	Leu	Leu	Thr	Phe	Cys	Val	Glu	His	His	Thr	Tyr	His	Ile	Lys	Asn
			85					90					95		
Tyr	Ile	Ile	Asn	Lys	Asp	Ile	Leu	Arg	Arg	Val	Leu	Val	Leu	Met	Ala
			100					105					110		
Ser	Lys	His	Ala	Phe	Leu	Ala	Leu	Cys	Ala	Leu	Arg	Phe	Lys	Arg	Lys
		115						120				125			
Ile	Ile	Gly	Leu	Lys	Asp	Glu	Phe	Tyr	Asn	Arg	Tyr	Ile	Met	Lys	Ser

130		135		140
Phe	Leu	Phe	Glu	Pro
145		150		155
Tyr	Asn	Leu	Met	Asn
		165		170
Val	Glu	Asp	Ile	Lys
		180		185
Lys	Ala	Leu	Glu	Asp
		195		200
Leu	Arg	Phe	Glu	Gln
		210		215
Ser	Met	Arg	Ser	Ile
		225		230
Thr	Leu	Glu	Asp	Glu
		245		250
Met	Glu	Asp	Gly	Glu
		260		265
Asp	Asp	Asp	Ile	Met
		275		280
Leu	Lys	Glu	Ser	Glu
		290		295
Gly	Arg	Gln	Ser	Pro
		305		310
Thr	Asn	Leu	Thr	Ser
		325		330
Gly	Ser	Pro	Gly	Ser
		340		345
Lys	Asn	Thr	Ser	Gln
		355		360
Gly	Leu	Val	Asp	Tyr
		370		375
Asp	Lys	Glu	Asp	Thr
		385		390
				395
				400

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 951 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

GCCAGGCAGG GTGTGGGGG AGCTGTGCCA ATCTACCTCA CAGGCCACC CCTGCCGGG 60  
CATGCCGTGG GATCATGGG AGGGAAGGCT CTGGGGGTG GAGACACCGC TGCTTAGCAC 120  
CCCCAGCCAG AACACCCTGA GGGTCTCGGG GCTCTGGAGA GAGTGGGGCG GGAGGAAGAA 180  
TGGCACCTT CCTAGGGAAG GAGACGAGCG CTTCGCCTTG ATTCTCCGAG AAGCCTCCGA 240  
GAAGTGCTTT AAGTGTGTTT GCATGCSCCA GCGGTGGGC AGCGGGGGCC TGTCARCCC 300  
TCTCCC GCCA TCCTCCCCA AGTGACGTCC ACTGCCTTGT CACGAGCGAC CTGCCTGTCA 360  
TGCCCCCCC CTGAGGAAGC ATGGGGACCC TAACACCCTG GTGCCCTGCA CCAGACAGGC 420  
CGTGGTCAGG CCCAGGCCAC CGGCCGGGTT CTGCCACARC TTCCACGTG CTGTCTGACA 480  
TGCSTGTGCC TGTGTGTGTT GTCTGTTGCT GTGTCGTGAA ACTGTGACCA TCACTCAGTC 540  
CAAACAAGTG AGTGGCCCTS GAGGCCACAG TTATGCAACT TTCAGTGTGT GTCATAACGA 600  
CGTCACTGCT TTTTAACTC GATAACTCTT TATTTTAGTA AAATGCCAG GAGTCTGGA 660  
AGCTACGCGG ACTTGACAGG GTTTTATTTT TTGGCCTTAG AATCTGCAGA AATTAGGAGG 720  
CACCGAGCCC AGCGCAGCAG CCTCGGACCC GGATGCGTTT TGCTTAGCG GATATGTTTA 780  
TACAGATGAA TATAAAATGT TTTTTCCTT GGGCTTTTGT CTCTTTTTC CCCCCCTTC 840  
TCACCTTCCC TTCTCCCTGA CCCCCCCCC CAAAAAAGCT ACTTCTTCAT TCCGTGGTAC 900  
GATTATTTTT TTTAACTAAA GGAAGATAAA ATTCTAAAAA AAAAAAAAAA A 951

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Met Pro Trp Asp His Gly Gln Gly Arg Leu Trp Gly Ser Glu Thr Pro  
1 5 10 15  
Leu Leu Ser Thr Pro Ser Gln Asn Thr Leu Arg Val Ser Gly Leu Trp  
20 25 30  
Arg Glu Trp Gly Gly Arg Lys Asn Trp His Leu Pro Arg Glu Gly Asp  
35 40 45

Glu Arg Phe Ala Leu Ile Leu Arg Glu Ala Ser Glu Lys Cys Phe Lys  
50 55 60

Cys Val Cys Met Xaa Gln Ala Val Gly Ser Gly Gly Leu Ser Xaa Pro  
65 70 75 80

Leu Pro Pro Ser Phe Pro Lys  
85

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1899 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GGCCGCTGT GTCCACGGGA CGCGGGCGGA TCTTCTCCGG CCATGAGGAA GCCAGCCGCT	60
GGCTTCCTTC CCTCACTCCT GAAGGTGCTG CTCCTGCCTC TGGCACCTGC CGCAGCCCCAG	120
GATTCGACTC AGGCCTCCAC TCCAGGCAGC CCTCTCTCTC CTACCGAATA CGAACGCTTC	180
TTTCGCACTG TGACTCCAAC CTGGAAGGCA GAGACTACCT GCCGTCTCCG TGCAACCCAC	240
GCCTGCCGGA ATCCCACTACT CGTCCAGCTG GACCAATATG AAAACCACGG CTTAGTGCCC	300
GATGGTGCTG TCTGCTCCAA CCTCCCTTAT GCCTCCTGGT TTGAGTCTTT CTGCCAGTTC	360
ACTCACTACC GTTGTCTCAA CCACGTCTAC TATGCCAAGA GAGTCTCTGTG TTCCCAGCCA	420
GTCTCTATTC TCTCACCTAA CACTCTCAAG GAGATAGAAG CTTCAGCTGA AGTCTCACCC	480
ACCACGATGA CCTCCCCCAT CTCACCCAC TTCAAGTGA CAGAAGGCCA GACCTTCCAG	540
CCCTGGCCTG AGAGGCTCAG CAACAACGTG GAAGAGCTCC TACAATCCTC CTTGTCCCTG	600
GGAGGCCAGG AGCAAGCGCC AGAGCACAAG CAGGAGCAAG GAGTGGAGCA CAGGCAGGAG	660
CCGACACAAG AACACAAGCA GGAAGAGGGG CAGAAACAGG AAGAGCAAGA AGAGGAACAG	720
GAAGAGGAGG GAAAGCAGGA AGAAGGACAG GGGACTAAGG AGGGACGGGA GGCTGTGTCT	780
CAGTGCAGA CAGACTCAGA GCCCAAGTTT CACTCTGAAT CTCTATCTTC TAACCTTCC	840
TCTTTTGCTC CCCGGGTACG AGAAGTAGAG TCTACTCCTA TGATAATGGA GAACATCCAG	900
GAGTCATTTC GATCAGCCCA GGAATAGAT GAAATGAATG AAATATATGA TGAGAACTCC	960
TACTGGAGAA ACCAAAACCC TGGCAGCCTC CTGCAGCTGC CCCACACAGA GGCCTTGCTG	1020
GTGCTGTGCT ATTCGATCGT GGAGAATACC TGCATCATAA CCCCACAGC CAAGGCCTGG	1080

AAGTACATGG AGGAGGAGAT CCTTGGTTTC GGGAAAGTCGG TCTGTGACAG CCTTGGGCGG 1140  
 CGACACATGT CTACCTGTGC CCTCTGTGAC TTCTGCTCCT TGAAGCTGGA GCAGTGGCCAC 1200  
 TCAGAGGCCA GCCTGCAGCG GCAACAATGC GACACCTCCC ACAAGACTCC CTTTGTGACG 1260  
 CCCTTGCTTG CCTCCCAGAG CCGTGCCATC GGCAACCAGG TAGGGTCCCC AGAATCAGGC 1320  
 CGCTTTTACG GGCTGGATTG GTACGGTGGG CTCCACATGG ACTTCTGGTG TGCCCGGCTT 1380  
 GCCACGAAAG GCTGTGAAGA TGTCGAGTGC TCTGGGTGGC TCCAGACTGA GTTCCTTAGC 1440  
 TTCCAGGATG GGGATTTCCT TACCAAGATT TGTGACACAG ACTATATCCA GTACCCAAAC 1500  
 TACTGTTCCT TCAAAAGCCA GCAGTGTCTG ATGAGAAACC GCAATCGGAA GGTGTCCCGC 1560  
 ATGAGATGTC TGCAGAATGA GACTTACAGT GCGCTGAGCC TGGCAAAAGT GAGGACGTTG 1620  
 TGCTTTCGAT GGAGCCAGGA GTTCAGCACC TTGACTCTAG GCCAGTTCGG ATGAGCTKGS 1680  
 GTTTATTTTG CCCACACCCC AGCCCAACCT GCCCAGTTC TCTATTGTTT TGAGACCCCA 1740  
 TTGCTTTCAG GCTGCCCTT CTGGGTCTGT TACTCGGCC CTAMTCACAT TTCCTTGGGT 1800  
 TGGAGCAACA GTCCCAGAGA GGGCCACGGT GGGAGCTGCG CCCTCCTTAA AAGATGACTT 1860  
 TACATAAAAT GTTGATCTTC AAAAAAAAAA AAAAAAAAAA 1899

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 543 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Met	Arg	Lys	Pro	Ala	Ala	Gly	Phe	Leu	Pro	Ser	Leu	Leu	Lys	Val	Leu
1				5					10				15		
Leu	Leu	Pro	Leu	Ala	Pro	Ala	Ala	Ala	Gln	Asp	Ser	Thr	Gln	Ala	Ser
		20						25					30		
Thr	Pro	Gly	Ser	Pro	Leu	Ser	Pro	Thr	Glu	Tyr	Glu	Arg	Phe	Phe	Ala
		35					40				45				
Leu	Leu	Thr	Pro	Thr	Trp	Lys	Ala	Glu	Thr	Thr	Cys	Arg	Leu	Arg	Ala
		50				55					60				
Thr	His	Gly	Cys	Arg	Asn	Pro	Thr	Leu	Val	Gln	Leu	Asp	Gln	Tyr	Glu
65					70					75				80	
Asn	His	Gly	Leu	Val	Pro	Asp	Gly	Ala	Val	Cys	Ser	Asn	Leu	Pro	Tyr
				85					90					95	

Ala Ser Trp Phe Glu Ser Phe Cys Gln Phe Thr His Tyr Arg Cys Ser  
 100 105 110  
 Asn His Val Tyr Tyr Ala Lys Arg Val Leu Cys Ser Gln Pro Val Ser  
 115 120 125  
 Ile Leu Ser Pro Asn Thr Leu Lys Glu Ile Glu Ala Ser Ala Glu Val  
 130 135 140  
 Ser Pro Thr Thr Met Thr Ser Pro Ile Ser Pro His Phe Thr Val Thr  
 145 150 155 160  
 Glu Arg Gln Thr Phe Gln Pro Trp Pro Glu Arg Leu Ser Asn Asn Val  
 165 170 175  
 Glu Glu Leu Leu Gln Ser Ser Leu Ser Leu Gly Gly Gln Glu Gln Ala  
 180 185 190  
 Pro Glu His Lys Gln Glu Gln Gly Val Glu His Arg Gln Glu Pro Thr  
 195 200 205  
 Gln Glu His Lys Gln Glu Glu Gly Gln Lys Gln Glu Glu Gln Glu Glu  
 210 215 220  
 Glu Gln Glu Glu Glu Gly Lys Gln Glu Glu Gly Gln Gly Thr Lys Glu  
 225 230 235 240  
 Gly Arg Glu Ala Val Ser Gln Leu Gln Thr Asp Ser Glu Pro Lys Phe  
 245 250 255  
 His Ser Glu Ser Leu Ser Ser Asn Pro Ser Ser Phe Ala Pro Arg Val  
 260 265 270  
 Arg Glu Val Glu Ser Thr Pro Met Ile Met Glu Asn Ile Gln Glu Leu  
 275 280 285  
 Ile Arg Ser Ala Gln Glu Ile Asp Glu Met Asn Glu Ile Tyr Asp Glu  
 290 295 300  
 Asn Ser Tyr Trp Arg Asn Gln Asn Pro Gly Ser Leu Leu Gln Leu Pro  
 305 310 315 320  
 His Thr Glu Ala Leu Leu Val Leu Cys Tyr Ser Ile Val Glu Asn Thr  
 325 330 335  
 Cys Ile Ile Thr Pro Thr Ala Lys Ala Trp Lys Tyr Met Glu Glu Glu  
 340 345 350  
 Ile Leu Gly Phe Gly Lys Ser Val Cys Asp Ser Leu Gly Arg Arg His  
 355 360 365  
 Met Ser Thr Cys Ala Leu Cys Asp Phe Cys Ser Leu Lys Leu Glu Gln  
 370 375 380  
 Cys His Ser Glu Ala Ser Leu Gln Arg Gln Gln Cys Asp Thr Ser His  
 385 390 395 400

Lys Thr Pro Phe Val Ser Pro Leu Leu Ala Ser Gln Ser Leu Ser Ile  
 405 410 415  
 Gly Asn Gln Val Gly Ser Pro Glu Ser Gly Arg Phe Tyr Gly Leu Asp  
 420 425 430  
 Leu Tyr Gly Gly Leu His Met Asp Phe Trp Cys Ala Arg Leu Ala Thr  
 435 440 445  
 Lys Gly Cys Glu Asp Val Arg Val Ser Gly Trp Leu Gln Thr Glu Phe  
 450 455 460  
 Leu Ser Phe Gln Asp Gly Asp Phe Pro Thr Lys Ile Cys Asp Thr Asp  
 465 470 475 480  
 Tyr Ile Gln Tyr Pro Asn Tyr Cys Ser Phe Lys Ser Gln Gln Cys Leu  
 485 490 495  
 Met Arg Asn Arg Asn Arg Lys Val Ser Arg Met Arg Cys Leu Gln Asn  
 500 505 510  
 Glu Thr Tyr Ser Ala Leu Ser Leu Ala Lys Val Arg Thr Leu Cys Phe  
 515 520 525  
 Arg Trp Ser Gln Glu Phe Ser Thr Leu Thr Leu Gly Gln Phe Gly  
 530 535 540

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 722 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

CGACCTTCCC AGCAATATGC ATCTTGACAG TCTGGTCGGC TCCTGCTCCC TCCTTCTGCT	60
ACTGGGGGCC CTGTCTGGAT GGGCGGCCAG CGATGACCCC ATTGAGAAGG TCAITGAAGG	120
GATCAACCGA GGGCTGAGCA ATGCAGAGAG AGAGGTGGGC AAGGCCCTGG ATGGCATCAA	180
CAGTGGAATC ACGCATGCCG GAAGGGAAGT GGAGAAGGTT TTCAACGGAC TTAGCAACAT	240
GGGGAGCCAC ACCGGCAAGG AGTTGGACAA AGGCGTCCAG GGGCTCAACC ACGGCATGGA	300
CAAGGTTGCC CATGAGATCA ACCATGGTAT TGGACAAGCA GGAAAGGAAG CAGAGAAGCT	360
TGGCCATGGG GTCAACAACG CTGTCTGGACA GGGCAACCAT CAAAGCGGAT CTTCCAGCCA	420
TCAAGGAGGG GCCACAACCA CGCCGTTAGC CTCTGGGGCC TCGGTCAACA CGCCTTTTAT	480
CAACCTTCCC GCCCTGTGGA GGAGCGTCGC CAACATCATG CCCTAAACTG GCATCCGGCC	540
TGTCTGGGAG AATAATGTCT CCGTTGTAC ATCAGCTGAC ATGACCTGGA GGGGTTGGGG	600



GTGGGGGACA GGTTCCTGAA ATCCCTGAAG GGGTTGTAC TGGGATTGT GAATAAACTT 660  
 GATACACTAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 720  
 AA 722

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 169 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Met His Leu Ala Arg Leu Val Gly Ser Cys Ser Leu Leu Leu Leu Leu  
 1 5 10 15  
 Gly Ala Leu Ser Gly Trp Ala Ala Ser Asp Asp Pro Ile Glu Lys Val  
 20 25 30  
 Ile Glu Gly Ile Asn Arg Gly Leu Ser Asn Ala Glu Arg Glu Val Gly  
 35 40 45  
 Lys Ala Leu Asp Gly Ile Asn Ser Gly Ile Thr His Ala Gly Arg Glu  
 50 55 60  
 Val Glu Lys Val Phe Asn Gly Leu Ser Asn Met Gly Ser His Thr Gly  
 65 70 75 80  
 Lys Glu Leu Asp Lys Gly Val Gln Gly Leu Asn His Gly Met Asp Lys  
 85 90 95  
 Val Ala His Glu Ile Asn His Gly Ile Gly Gln Ala Gly Lys Glu Ala  
 100 105 110  
 Glu Lys Leu Gly His Gly Val Asn Asn Ala Ala Gly Gln Gly Asn His  
 115 120 125  
 Gln Ser Gly Ser Ser Ser His Gln Gly Gly Ala Thr Thr Thr Pro Leu  
 130 135 140  
 Ala Ser Gly Ala Ser Val Asn Thr Pro Phe Ile Asn Leu Pro Ala Leu  
 145 150 155 160  
 Trp Arg Ser Val Ala Asn Ile Met Pro  
 165

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1240 base pairs  
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

AATGGCTTTT CTTCCTTCCT GGGTTTGTGT ACTAGTTGGT TCCTTTTCTG CTTCCTTAGC	60
AGGGACTTCC AATCTCTCAG AGACAGAGCC CCCTCTGTGG AAGGAGAGTC CTGGTCAGCT	120
CAGTGACTAC AGGGTGGAGA ACAGCATGTA CATTATTAAT CCCTGGGTAT ACCTTGAGAG	180
AATGGGGATG TATAAAATCA TATTGAATCA GACAGCCAGG TATTTTGCAA AATTTCACCC	240
AGATAATGAA CAGAATATTT TATGGGGGTT GCCTCTGCAG TATGGCTGGC AATATAGGAC	300
AGGCAGATTA GCTGATCCAA CCCGAAGGAC AAAGTGTGGC TATGAATCTG GAGATCATAT	360
GTGCATCTCT GTGACAGTT GGTGGGCTGA TTTGAATTAT TTTCTGTCTT CATTACCCCTT	420
TCTTGCTGCG GTTGATTCTG GTGTAATGGG GATATCATCA GACCAAGTCA GGCTTTTGCC	480
CCCACCCAG AATGAGAGGA AGTTTTGTGA TGATGTTTCT AGCTGTCGTT CATCCTTCCC	540
TGAGACAATG AACAAAGTGA ACACCTTTTA CCAGTATTG CAGTCACCTT TTAGTAAGTT	600
TGATGATCTG TTGAAGTACT TATGGGCTGC ACACACTTCA ACCTTGCGAG ATAATATCAA	660
AAGTTTGTAA GACAGATATG ATTATTATTC TAAAGCAGAA GCGCATTTTG AGAGAAGTTG	720
GGTACTGGCT GTGGATCATT TAGCTGCAGT CCTCTTTCCT ACAACCTTGA TTAGATCATA	780
TAAGTCCAG AAGGGCATGC CACCACGAAT TCTTCTTAAT ACTGATGTAG CCCCTTTCAT	840
CAGTGACTTT ACTGCTTTTC AGAATGTAGT CCTGGTTCTT CTAAATATGC TTGACAATGT	900
GGATAAATCT ATAGGTTATC TTTGTACAGA AAAATCTAAT GTATATAGAG ATCATTGCGA	960
ATCTAGCTCT AGAAGTTATG GAAATAACTC CTGAAACATT TAACTTCAAA CTTGAGGAAA	1020
TGATTAATGA ATTAATAATG AAAAAGTCGA ACTTGACAA CAGTAATTTC AAAAAATTA	1080
TGTCATCATG ACCATGTAGT TTATTCCTTC TGATATTTT GATTATGCT TATTTGTTAA	1140
GATCTTGATC ATGTATTAAA AACTTAAATT AAATGCATTC AAGTTAAAAA AAAAAAATA	1200
AAAAAATAAA AAAAAAATAA AAAAAAATAA AAAAAAATAA	1240

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 330 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

09746783.132400

**2007-08**

**2007-08**

Val Val Leu Val Leu Leu Asn Met Leu Asp Asn Val Asp Lys Ser Ile  
290 295 300

Gly Tyr Leu Cys Thr Glu Lys Ser Asn Val Tyr Arg Asp His Ser Glu  
305 310 315 320

Ser Ser Ser Arg Ser Tyr Gly Asn Asn Ser  
325 330

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2261 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GCAGCACCAG CCGTCTGCAG CTCGCGCCGC CACTTGCGCC TCTCCAGCCT CCGCAGGCC	60
AACCGCCGCC AGCACCATGG CCAGCACCAT TTCGCGCTAC AAGGAGAAGA TGAAGGAGCT	120
GTGGGTGCTG TCGCTCATCT GCTCCTGCTT CTACACACAG CCGCACCCCA ATACCGTCTA	180
CCAGTACGGG GACATGGAGG TGAAGCAGCT GGACAAGCGG GCCTCAGGCC AGAGCTTCGA	240
GGTCATCCTC AAGTCCCTT CTGACCTGTC CCCAGAGAGC CCTATGCTCT CCTCCCCACC	300
CAAGAAGAAG GACACCTCCC TGGAGGAGCT GCAAAAGCGG CTGGAGGCAG CCGAGGAGCG	360
GAGGAAGACG CAGGAGGCGC AGGTGCTGAA GCAGCTGGCG GAGCGGCGCG AGCACGAGCG	420
CGAGGTGCTG CACAAGGCGC TGGAGGAGAA TAACAATCTC AGCCGCCAGG CGGAGGAGAA	480
GCTCAACTAC AAGATGGAGC TCAGCAAGGA GATCCGCGAG GCACACCTGG CCGCACTGCG	540
CGAGCGGCTG CGCGAGAAGG AGCTGCACGC GGCCGAGGTG CGCAGGAACA AGGAGCAGCG	600
AGAAGAGATG TCGGGCTAAG GGCCCCGGAC GGGCGGCGCC CATCTGCGA CAGAACACGT	660
TCGGGTTTTT GTTTTGTTC GTTCACCTCT GTCTAGATGC AACTTTTGTT CCTCTCCCC	720
CACCCAGCC CCCAGCTTCA TGCTTCTCTT CCGCACTCAG CCGCCCTGCC CTGTCTCTCT	780
GGTGAGTCGC TGACCAAGGC TTCCCCTGCA GGAGCCGCGG GCGGTGAGAC GCGGTCCCTC	840
GGTGCAGACA CCAGGCCGGG CGCGGCTGGG TCCCCCGGGG GCCCTGTGAG AGAGGTGGCG	900
GTGACCGTGG TAAACCCAGG CCGGTGGCGT GGGATCGCGG GTCTTACGC TGGGCTGTCT	960
GGTCAGCACG TGCAGGTCAG GGCAGGTCCT CTGAGCCGCG GCCCTGGCC AGCAGGCGAG	1020
GCTACAGTAC CTGCTGTCTT TCCAGGGGGA AGGGGCTCCC CATGAGGGAG GGGCGACGGG	1080

GGAGGGGGGT GATGTCCT GGGAGCCTGC GTGTGCAGCC GGTGCTTGT GAAGTGGCAG 1140  
 GCGGGTGGGT GGGGCTGCA GCTTTCCTTA ATGTGGTTGC ACAGGGGTCC TCTGAGACCA 1200  
 CCTGGCGTGA GGTGGACACC CTGGGCTTC CTGGAAGCCT GCAGTTGGGG GCCTGCCCTG 1260  
 AGTCTGCTGG GGAGTGGCA TTCTCTGCCA GGGACCCATG AGCAGGCTGC ATGGTCTAGA 1320  
 GGTGTGGGC AGCATGGACA GTCCCCACT CAGAAGTGCA AGAGTCCAA AGAGCCTCTG 1380  
 GCCAGGCCC CTCCCCACCA GGGCTTTGCA GATGTCTTGG AAAGACCCAC CCTAGAGCCC 1440  
 TTTGAGTGC TGGCCCTCC TGTGCCCTCT GCCCTGGTGG AAGCGGCAGC CACAAGTCTT 1500  
 CCTCAGGAG CCCAAGGGG GATTTTGTGG GACCGCTGCC CACAGATCCA GGTGTTGGAA 1560  
 GGGCAGCGGG TAAGGTTCCC AAGCCAGCCC CAACACCCCT CCCACTTGGC ACCCAGAGGG 1620  
 GGCTGTGGGT GGAGGCCTGA CTCAGGCCT CTCCTGCCCA CACCCTCTGG GCTGAGTTC 1680  
 TTCTTTCCCT TGGACGCCCA GTGCTGGCCT TGGAGGACGG TCAGCTGGAG GATGGCGGTG 1740  
 GGGGAGGCTG TCTTTGTACC ACTGCAGCAT CCCCCACTTC TCCACGGAAG CCCCATCCCA 1800  
 AAGCTGTGTC CTGGCCCTT GCTGTAAAGT GTGAAGGGGG CGGCTGAGTT CTCTTAGGAC 1860  
 CCAGAGCCAG GGCCCTCAAC TTCCATCTGT CGGGAGGCTT TGGCCGGGCA CTGCCAGTGT 1920  
 CTTCCAGAGC CACACCCAGG GACCACGGGA GGATCTGAC CCCTGCAGGG CTCAGGGGTC 1980  
 AGCAGGGACC CACTGCCCCA TCTCCCTCTC CCCACCAAGA CAGCCCCAGA AGGAGCAGCC 2040  
 AGCTGGGATG GGAACCAAG GCTGTCCACA TCTGGCTTTT GTGGGACTCA GAAAGGGAAG 2100  
 CAGAACTGAG GGCTGGGATA TTCTCATG GGCAGCGCT CATAGCGAAA GCCTACTGTA 2160  
 ATATGCACCC ATCTCATCCA CGTAGTAAAG TGAACITAAA AAITCAATCA AATGAACAAT 2220  
 TAAATAAACA CCTGTGTGTT TAAGAAAAAA AAAAAAAAAA A 2261

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 180 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Met	Ala	Ser	Thr	Ile	Ser	Ala	Tyr	Lys	Glu	Lys	Met	Lys	Glu	Leu	Ser
1					5				10				15		
Val	Leu	Ser	Leu	Ile	Cys	Ser	Cys	Phe	Tyr	Thr	Gln	Pro	His	Pro	Asn
			20					25					30		

Thr Val Tyr Gln Tyr Gly Asp Met Glu Val Lys Gln Leu Asp Lys Arg  
 35 40 45  
 Ala Ser Gly Gln Ser Phe Glu Val Ile Leu Lys Ser Pro Ser Asp Leu  
 50 55 60  
 Ser Pro Glu Ser Pro Met Leu Ser Ser Pro Pro Lys Lys Lys Asp Thr  
 65 70 75 80  
 Ser Leu Glu Glu Leu Gln Lys Arg Leu Glu Ala Ala Glu Glu Arg Arg  
 85 90 95  
 Lys Thr Gln Glu Ala Gln Val Leu Lys Gln Leu Ala Glu Arg Arg Glu  
 100 105 110  
 His Glu Arg Glu Val Leu His Lys Ala Leu Glu Glu Asn Asn Asn Phe  
 115 120 125  
 Ser Arg Gln Ala Glu Glu Lys Leu Asn Tyr Lys Met Glu Leu Ser Lys  
 130 135 140  
 Glu Ile Arg Glu Ala His Leu Ala Ala Leu Arg Glu Arg Leu Arg Glu  
 145 150 155 160  
 Lys Glu Leu His Ala Ala Glu Val Arg Arg Asn Lys Glu Gln Arg Glu  
 165 170 175  
 Glu Met Ser Gly  
 180

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3109 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GGCCAAAGAG GCCTAGGAGC CTCGTGGCTG CGTCACCGCC GCCCCCCCAG ACAAGATGGA	60
CACCGCGGAG GAAGACATAT GTAGAGTGTG TCGGTCAGAA GGAACACCTG AGAAACCGCT	120
TTATCATCCT TGTGTATGTA CTGGCAGTAT TAAGTTTATC CATCAAGAAT GCTTAGTTCA	180
ATGGCTGAAA CACAGTCGAA AAGAACTACTG TGAATTATGC AAGCACAGAT TTGCTTTTAC	240
ACCAATTAT TCTCCAGATA TGCCCTCAGC GCTTCCAATT CAAGACATAT TTGCTGGACT	300
GGTTACAAGT ATTGGCACTG CAATACGATA TTGGTTTCAT TATACACTTG TGGCCTTTGC	360
ATGGTTGGGA GTTGTTCCTC TTACAGCATG CCGCATCTAC AAGTGCTTGT TTACTGGCTC	420
CCGTAGAGTC ACTACTGACG CTGCCCATTA GATATGCTGT CAACCGGAAA ATTTGTTGGC	480

AGATGTGTTG CAGGGTTGTT TTGTGGTGAC GTGCACACTG TGTGCATTCA TCAGCCTGGT	540
GTGGTTGAGA GAGCAGATAG TCCATGGGGG AGCACCAATT TGTTGGAGC ATGCTGCCCC	600
ACCGTTCAAT GCTGCGGGG ATCACCAAAA TGAGGCTCCA GCAGGAGGAA ATGGTGCAGA	660
AAATGTTGCT GCTGATCAGC CTGCTAACC ACCAGCTGAG AACGCAGTGG TGGGGGAAAA	720
CCCTGATGCC CAGGATGACC AGGCAGAAGA GGAGGAGGAG GACAATGAGG AGGAAGATGA	780
CGCTGGTGTG GAGGATGGCG GCAGATGCTA ATAACGGAGC CCAGGATGAC ATGAATTGGA	840
ATGCTTTAGA ATGGGACCGA GCTGCTGAAG AGCTTACATG GGAAAGAATG CTAGGACTTG	900
ATGGATCACT AGTTTTTCTG GAACATGTCT TCTGGTGGT ATCTTTAAAT ACACGTTC	960
TTCTTGTTTT TGCATTTTGC CCTTACCATA TTGGTCATT CTCCCTTGT GGTTTGGGAT	1020
TTGAAGAACA CGTCCAAGCA TCTCATTTTG AAGGCCTAAT CACAACCATA GTTGGGTATA	1080
TACTTTTAGC AATAACACTG ATAATTTGTC ATGGCTTGGC AACTCTTGTG AAATTCATA	1140
GATCTCGTCG CTTACTGGGA GTCTGTATA TTGTTGTTAA GGCTCTTTG TTAGTGGTGG	1200
TAGAAATTGG AGTATTCCT CTCATTTGTG GTTGGTGGCT GGATATCTGT TCCTTGGAAA	1260
TGTTTGATGC TACTCTGAAA GATCGAGAAC TGAGCTTCCA GTCGGCTCCA GGTACTACCA	1320
TGTTTCTGCA TTGGCTAGTG GGAATGGTAT ATGTCTTCTA CTTTGCCTCC TTCATTCTAT	1380
TACTGAGAGA GGTACTTCGA CCTGTGTGCC TGTGGTTTCT AAGGAATTTG AATGATCCAG	1440
ATTTCAATCC AGTACAGGAA ATGATCCATT TGCCAATATA TAGGCATCTC CGAAGATTTA	1500
TTTGTCTAGT GATTGTCTTT GGCTCCATTG TCCTCTGAT GCTTTGGCTT CCTATACGTA	1560
TAATTAAGAG TGTGCTGCCT AATTTTCTTC CATACAATGT CATGCTCTAC AGTGATGCTC	1620
CAGTGAGTGA ACTGTCCCTC GAGCTGCTTC TGCTTCAGGT TGCTTGCCA GCATTACTCG	1680
AACAGGGACA CACGAGGACG TGCTGAAGG GGCTGGTGGC AGCGTGGACT GTGACCGCCG	1740
GATACTTGCT GGATCTTCAT TCTTATTAT TGGGAGACCA GGAAGAAAAT GAAAACAGTG	1800
CAAAATCAACA AGTTAACAAT AATCAGCATG CTCGAAATAA CAACGCTATT CCTGTGGTGG	1860
GAGAAGGCCT TCATGCAGCC CACCAAGCCA TACTCCAGCA GGGAGGGCCT GTTGGCTTTC	1920
AGCCTTACCG CCGACCTTTA AATTTTCCAC TCAGGATATT TCTGTTGATT GTCTTCATGT	1980
GTATAACATT ACTGATTGCC AGCCTCATCT GCCTTACTTT ACCAGTATTT GCTGGCCGTT	2040
GGTTAATGTC GTTTTGAGCG GGGACTGCCA AAATCCATGA GCTCTACACA GCTGCTTGTG	2100
GTCTCTATGT TTGCTGGCTA ACCATAAGGG CTGTGACGGT GATGTGGCA TGGATGCCTC	2160
AGGGACGCAG AGTGATCTTC CAGAAGGTTA AAGAGTGGTC TCTCATGATC ATGAAGACTT	2220

TGATAGTTGC GGTGCTGTTG GCTGGAGTTG TCCCTCTCCT TCTGGGGCTC CTGTTTGAGC	2280
TGGTCATTGT GGCTCCCCCTG AGGGTTCCCT TGGATCAGAC TCCTCTTTTT TATCCATGGC	2340
AGGACTGGGC ACTTGGAGTC CTGCATGCCA AAATCATTGC AGCTATAACA TTGATGGGTC	2400
CTCAGTGGTG GTTGAAAACT GTAATTGAAC AGGTTTACGC AAATGGCATC CGGAACAATTG	2460
ACCTTCACTA TATTGTTTCTG AAATGGGCAG CTCCCGTGAT CTCTGTGCTG TTGCTTTCCC	2520
TGTGTGTACC TTATGTCATA GCTTCTGGTG TTGTTCCCTT ACTAGGTGTT ACTGCGGAAA	2580
TGCAAAACTT AGTCCATCGG CGGATTATC CATTTTTACT GATGGTCGTG GTATTGATGG	2640
CAATTTTGTC CTTCCAAGTC CGCCAGTTTA AGCGCCTTTA TGAACATATT AAAAATGACA	2700
AGTACCTTGK GGGTCAASGA CTCGGTGAAC TACGAACGGA AATCTGGGCA AACAAGGCTC	2760
ATCTCCACCA CCTCCACAGT CATCCCAAGA ATAAAGTAGT TGTCTCAACA ACTTGACCTT	2820
CCCCTTTACA TGTCCTTTTT TGTGGACTTC TCTCTTKGGA GATTTTTCCC AGTGATCTCT	2880
CAGCGTKGTT TTTAAGTTAA AKGTATTGGA CTGTGTCTT CAGCATTGAG AGAGCAGCGG	2940
TGTAAGATTC TGCTGTTCTC CCTGGATCTT CTGACATKAC TGCTGTCTGA GATTTGTATA	3000
TGKGTAATA CAAGTTCCTT GATACCCATA AACCTTGAT TAAACAGAAT GTGCATKGTA	3060
CATCTTTAAA CAAAATGKAT ATTAATTTAT TAAAAAATA AAAAAAATA	3109

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 750 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Met	Gly	Glu	His	Gln	Phe	Gly	Trp	Ser	Met	Leu	Pro	His	Arg	Ser	Met
1				5					10					15	
Leu	Arg	Gly	Ile	Thr	Lys	Met	Arg	Leu	Gln	Gln	Glu	Glu	Met	Val	Gln
			20					25					30		
Lys	Met	Leu	Leu	Leu	Ile	Ser	Leu	Leu	Thr	His	Gln	Leu	Arg	Thr	Gln
			35					40					45		
Trp	Trp	Gly	Lys	Thr	Leu	Met	Pro	Arg	Met	Thr	Arg	Gln	Lys	Arg	Arg
			50			55					60				
Arg	Arg	Thr	Met	Arg	Arg	Lys	Met	Thr	Leu	Val	Trp	Arg	Met	Ala	Ala
65						70					75			80	



Asp Ala Asn Asn Gly Ala Gln Asp Asp Met Asn Trp Asn Ala Leu Glu  
 85 90 95  
 Trp Asp Arg Ala Ala Glu Glu Leu Thr Trp Glu Arg Met Leu Gly Leu  
 100 105 110  
 Asp Gly Ser Leu Val Phe Leu Glu His Val Phe Trp Val Val Ser Leu  
 115 120 125  
 Asn Thr Leu Phe Ile Leu Val Phe Ala Phe Cys Pro Tyr His Ile Gly  
 130 135 140  
 His Phe Ser Leu Val Gly Leu Gly Phe Glu Glu His Val Gln Ala Ser  
 145 150 155 160  
 His Phe Glu Gly Leu Ile Thr Thr Ile Val Gly Tyr Ile Leu Leu Ala  
 165 170 175  
 Ile Thr Leu Ile Ile Cys His Gly Leu Ala Thr Leu Val Lys Phe His  
 180 185 190  
 Arg Ser Arg Arg Leu Leu Gly Val Cys Tyr Ile Val Val Lys Val Ser  
 195 200 205  
 Leu Leu Val Val Val Glu Ile Gly Val Phe Pro Leu Ile Cys Gly Trp  
 210 215 220  
 Trp Leu Asp Ile Cys Ser Leu Glu Met Phe Asp Ala Thr Leu Lys Asp  
 225 230 235 240  
 Arg Glu Leu Ser Phe Gln Ser Ala Pro Gly Thr Thr Met Phe Leu His  
 245 250 255  
 Trp Leu Val Gly Met Val Tyr Val Phe Tyr Phe Ala Ser Phe Ile Leu  
 260 265 270  
 Leu Leu Arg Glu Val Leu Arg Pro Gly Val Leu Trp Phe Leu Arg Asn  
 275 280 285  
 Leu Asn Asp Pro Asp Phe Asn Pro Val Gln Glu Met Ile His Leu Pro  
 290 295 300  
 Ile Tyr Arg His Leu Arg Arg Phe Ile Leu Ser Val Ile Val Phe Gly  
 305 310 315 320  
 Ser Ile Val Leu Leu Met Leu Trp Leu Pro Ile Arg Ile Ile Lys Ser  
 325 330 335  
 Val Leu Pro Asn Phe Leu Pro Tyr Asn Val Met Leu Tyr Ser Asp Ala  
 340 345 350  
 Pro Val Ser Glu Leu Ser Leu Glu Leu Leu Leu Gln Val Val Leu  
 355 360 365  
 Pro Ala Leu Leu Glu Gln Gly His Thr Arg Gln Trp Leu Lys Gly Leu  
 370 375 380

Val	Arg	Ala	Trp	Thr	Val	Thr	Ala	Gly	Tyr	Leu	Leu	Asp	Leu	His	Ser
385					390					395					400
Tyr	Leu	Leu	Gly	Asp	Gln	Glu	Glu	Asn	Glu	Asn	Ser	Ala	Asn	Gln	Gln
				405					410					415	
Val	Asn	Asn	Asn	Gln	His	Ala	Arg	Asn	Asn	Asn	Ala	Ile	Pro	Val	Val
				420					425				430		
Gly	Glu	Gly	Leu	His	Ala	Ala	His	Gln	Ala	Ile	Leu	Gln	Gln	Gly	Gly
				435					440				445		
Pro	Val	Gly	Phe	Gln	Pro	Tyr	Arg	Arg	Pro	Leu	Asn	Phe	Pro	Leu	Arg
						455						460			
Ile	Phe	Leu	Leu	Ile	Val	Phe	Met	Cys	Ile	Thr	Leu	Leu	Ile	Ala	Ser
465					470					475					480
Leu	Ile	Cys	Leu	Thr	Leu	Pro	Val	Phe	Ala	Gly	Arg	Trp	Leu	Met	Ser
					485					490				495	
Phe	Trp	Thr	Gly	Thr	Ala	Lys	Ile	His	Glu	Leu	Tyr	Thr	Ala	Ala	Cys
				500					505				510		
Gly	Leu	Tyr	Val	Cys	Trp	Leu	Thr	Ile	Arg	Ala	Val	Thr	Val	Met	Val
							520						525		
Ala	Trp	Met	Pro	Gln	Gly	Arg	Arg	Val	Ile	Phe	Gln	Lys	Val	Lys	Glu
						535					540				
Trp	Ser	Leu	Met	Ile	Met	Lys	Thr	Leu	Ile	Val	Ala	Val	Leu	Leu	Ala
545					550					555					560
Gly	Val	Val	Pro	Leu	Leu	Leu	Gly	Leu	Leu	Phe	Glu	Leu	Val	Ile	Val
					565					570				575	
Ala	Pro	Leu	Arg	Val	Pro	Leu	Asp	Gln	Thr	Pro	Leu	Phe	Tyr	Pro	Trp
								585					590		
Gln	Asp	Trp	Ala	Leu	Gly	Val	Leu	His	Ala	Lys	Ile	Ile	Ala	Ala	Ile
								600					605		
Thr	Leu	Met	Gly	Pro	Gln	Trp	Trp	Leu	Lys	Thr	Val	Ile	Glu	Gln	Val
						615					620				
Tyr	Ala	Asn	Gly	Ile	Arg	Asn	Ile	Asp	Leu	His	Tyr	Ile	Val	Arg	Lys
625					630					635					640
Leu	Ala	Ala	Pro	Val	Ile	Ser	Val	Leu	Leu	Leu	Ser	Leu	Cys	Val	Pro
					645					650				655	
Tyr	Val	Ile	Ala	Ser	Gly	Val	Val	Pro	Leu	Leu	Gly	Val	Thr	Ala	Glu
								665					670		
Met	Gln	Asn	Leu	Val	His	Arg	Arg	Ile	Tyr	Pro	Phe	Leu	Leu	Met	Val
								680					685		

Val Val Leu Met Ala Ile Leu Ser Phe Gln Val Arg Gln Phe Lys Arg  
 690 695 700  
 Leu Tyr Glu His Ile Lys Asn Asp Lys Tyr Leu Xaa Gly Gln Xaa Leu  
 705 710 715 720  
 Gly Glu Leu Arg Thr Glu Ile Trp Ala Asn Lys Ala His Leu His His  
 725 730 735  
 Leu His Ser His Pro Lys Asn Lys Val Val Val Ser Thr Thr  
 740 745 750

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

TNTTTGAAGT TTCTCCCTCT CATCTCTGAG

29

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GNTTCTCCAC GTAGTTGGTT TTCCTCAGT

29

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

CNACATGACG TGAGCTGGTG ATCCATGAA

29

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

ANTTGGGCTC TGCCGTCCAG AAAGTTTG

29

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GNAGCTACGC GGACTTGCAG AGGTTTTAT

29

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

TNGGTGAGAG AATAGAGACT GGCTGGGAA

29

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

ANGAGCCGAC CAGACGTGCA AGATGCATA

29

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

ANCTGACCAG GACTCTCCTT CCACAGAGG

29

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

TNTAGGCGGA AATGGTGCTG GCCATGGTG

29

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:  
ANATATCCAG CCACCAACCA CAAATGAGA

29

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

GCTAATTGGA GAAGAAAACA AGTAGGATTT TTGTTTTGTT TTGCATTTTG CAATATGGAG	60
GAGAAATGAT TAGACCTTAG GAAGTGCCAG TGGGTGATC CTTCATGAA CATGCCATCA	120
GTAAAAGCCC TGGAAACAAG GTCATACCAG AGATTCATTG TGCCTGTCA CAACIGCAAA	180
CAATATCTGA GTGGAATATT CAAAACTTG CTTAGAAAGA AACTCTAGG ACAGATGGCT	240
CCACTGAAGT TATCCAAAT ATTTAATAAA TAAAGCATAC CAGGCTTTTA TAAACTCTTC	300
TAGAAGAAAA AAGTTGGAAT TTTTCCAATT CAGTTTTCAT GGCCAGTGCA ACCTTGATAC	360
CAAAACCAAT AAAACAACA AACAAACAAA AACATAAAG CTATAGACCA AAGTCTCATA	420
GATTTAGATG CAAATCCTTA AAATTGAAAA AAAAAGTCTA GTCATATCCA TAAACTGTAT	480
CATCACCAAG AGATGTTTAT TAGGGCAATC AAAAGATGAT TTATTATTTT TTAATAAATC	540
AATGTGGCCT TCCCTTCCCTC TTTCTTTTGA TTCCCCTCTT TGAGTTTFTA TGTGTCTCTT	600
TTGCCTTCCC TTCCCAGAGT GGAGGAGTGA GACCTGCATT GTGGGATGAG AGGAGTTGTG	660
GCTATGTGTC TGCTGGCACC AAGAGGGCTG AGGGTGAGGT GTGGAAGGGA CAGGGGGAGG	720
AGATGGGCAG CATTGTTAAG AGATTGGTAC CACTGAGCAA ATATGTTGAG AATGATGATG	780

GCAAGGTTTC TCCCTGTTAG AGAAGGTATT TGTAGAAATA GGAATGAGGA GAGCTAGAAA 840  
 ACCTGGAGTG TGGGATTAGA ATAGAACTCA TATCTTTTAA ATACATAGGA ACAATAGAGA 900  
 AATTGTGTGG TGTGCCCAT TACATATATT TTGTGATTCA TTCTACCGAG AGGACATAAA 960  
 TGCAGTCACA GCTCAGTAAC AGTAAACACA CCAACTGCCA AGTTATTATT TCCTAAATAC 1020  
 TATCCACAAA AAAGGGGACC AGGGATGATT CCTAGTCGGA GATTGGGAGA AAAAGAAGAT 1080  
 GAGCCTGAAT CATTTCATGT ACCTAACAGA AAGAAAATAC TCTGGCTGGG CTCAGWGGCT 1140  
 CATGTTTGTA ATTCTAGCAT GTTAGGAGGT CGAGGTGGGT GTGTTGCTTG AGCCCAGGAG 1200  
 TTTGAGACCA GCCCAGGCAA CATGGCAAAA CTGTCTCTAC AAAAAATATA AAAGTTAGCC 1260  
 AGGCGTGGT GCATGCGCCT GTCGTCGAG ATACTCGGA GGCAGAGAGG TGGGAGGATC 1320  
 ACTTGAGCCT GGGAGATTGA GACTGCATCG AGCTGTGGTC ATGCCACTGC ACTCCAGCCT 1380  
 GGAGGACAGA GTGAGACCCT GTCTCAGGAA AAAAAAAAAA AAAAA 1425

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 94 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Met	Ile	Tyr	Tyr	Phe	Leu	Lys	Asn	Gln	Cys	Gly	Leu	Pro	Phe	Leu	Phe
1				5				10					15		
Leu	Leu	Ile	Pro	Leu	Phe	Glu	Phe	Leu	Cys	Val	Ser	Phe	Ala	Phe	Pro
			20					25					30		
Ser	Gln	Ser	Gly	Gly	Val	Arg	Pro	Ala	Leu	Trp	Asp	Glu	Arg	Ser	Cys
			35				40					45			
Gly	Tyr	Val	Ser	Ala	Gly	Thr	Lys	Arg	Ala	Glu	Gly	Glu	Val	Trp	Lys
			50				55					60			
Gly	Gln	Gly	Glu	Glu	Met	Gly	Ser	Ile	Val	Lys	Arg	Leu	Val	Pro	Leu
			65			70				75				80	
Ser	Lys	Tyr	Val	Glu	Asn	Asp	Asp	Gly	Lys	Val	Ser	Pro	Cys		
					85				90						

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2859 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

CGCACCCAGC CGCGCCGGCG AGGACATGGG CAGCCCGGCG GCGCCACCC CCCGCGCCGA	60
TGTGAATTAT TAAAAAGAAA ATGGCCCCAAC GGAGCACTGT ATTTCTTCT CGTGTCACCA	120
AGGAAAGGTA TAATATATGG AAAATATGCA TCTAAGGCGA GTGAGAACCA TGCCCCGACA	180
CAGCCAGTCC CTGACCATGG CACCATACTC ATCTGTAAGC CTCGTGGAGC AGCTGGAAGA	240
CAGGATCCTC TGCCATGAGA AAACCACCGC CGCCCTCGTA GAGCACGCCT TTCGGATTAA	300
AGATGACATT GTCAACAGTT TGCAGAAAAT GCAAAACAAA GGGGGAGGTG ACCGCTTGGC	360
CAGGCTTTTC TTGGAGGAGC ATATCAGAAA CATAACTGCC ATAGTGAAGC AACTTAATCG	420
GGATATCGAG GTACTCCAGG AGCAGATTGC TGCTCGGAC AACATTAGCT ATGGAACATA	480
TTCTGCCTTA AAGACCCTGG AGATGCGCCA GCTCTCCGGT TTGGGAGATC TTCAGGAAG	540
AGTGGCAAGA TGTGATGCCA GCATAGCTAG ACTTTCTGCA GAGCACAAAA CGACCTATGA	600
GGGGCTCCAG CACTTGAACA AAGAACAGCA GGTGCGCAAA CTATCTTGG AAACGAAAAT	660
CAAAGATGCA GAGGGACAGA TTTCTCAGCT TTTGAACAGA GTGGACTTGT CAATATCAGA	720
GCAGAGCACC AAAGTGAAGA TGTCTCACAG AGACAGTAAC CACCAGCTTC AGCTTTTGGA	780
CACTAAATTT AAAGGTACAG TTGAGGAACT CAGTAACGAG ATATTATCTG CACGGAGTTG	840
GTTGCAACAG GAACAAGAAC GGATAGAAAA AGAGCTTTTA CAGAAAATTG ATCAGCTTTC	900
CTTGATTGTT AAGGAAAACA GTGGAGCCAG TGAAGGGAT ATGGAGAAGA AGCTCAGCCA	960
GATGTCAGCC AGGCTTGACA AAATAGAAGA GGGTCAAAAG AAGACTTTTG ATGGTCAGAG	1020
AACAAGGCAA GAAGAGGAGA AGATGCACGG GCGAATCACC AAGCTGGAGT TACAGATGAA	1080
CCAGAACATC AAGGAAATGA AAGCAGAAGT TAATGCTGGG TTTACAGCCG TCTATGAAAG	1140
CATAGGATCC CTCAGGCAAG TTCTCGAGGC CAAGATGAAG CTGGACAGGG ACCAGCTACA	1200
GAAGCAAATC CAGCTGATGC AGAAGCCAGA GACCCCATG TGAAGGGAGC TGGACAAGG	1260
TCCTAAAAGA CAGTTTGGCC AGTGGGGCTA GGAGCCGGAT ACCTCTGTAG CCAGGCCATC	1320
GCTGCATTCA GGATTGTTC ATCCATGGCG TGCATGTGCC AAGAAATGTG TTTTATGGG	1380
TCTAAATGTT TACCTTGAGT CTTGAAAATA CTCTTTTGTT AAAAGTATGA AATACAGTTT	1440

09746733-123100



TTACCAGTTT ATTTCAC TTC TCTAAATTC A ATGGAATCC CCCGCCCTGG ATTTTGAAAG	1500
GCTTTTATCT TCTTCATTTT ACGAATGGAA AGACGACAAT TTTTCTTCAA TGCTTGATGC	1560
ACTAATGAAG ACTGTTTACT ATTTTGAAAA ATGTCATGGG GATTTTTTTT TAATTAAGAA	1620
ACTAATGAAT CATCACAGGA ATGTGTGTCT CCTCACCTTA AATTAAGAGA ATGTCCCAGT	1680
AGATTAGACT TCAACCTTGG AGTCCAAATTT GGATTTTATT ATCGTTGICT ATGCACTTCT	1740
TATATTGGTT ATCTTCTTGT AAATCTTCTG TCTTTTGTA GGGGAAAGGA TTTAACATTT	1800
AGAATAAAC CCACCATTTA TGTAATGGAA ATAGTTTAAA AATTGCTAAC TGCCATGTGG	1860
ATTGCAAAT AAATGGAAAC TTATTTAGAT AACGTAAGGC TCAATATCTG CGTTGACCAC	1920
CTAGATATTA CAGGTTTTAA TATTTAAAC TATTTTGAA TTATCCACA CCTGTATAGT	1980
GATAGCCATA TATTTAATAA TGGAAATGGT GTTAACAGTC TATTTACTGC ACAATTAATT	2040
GTTCACTAAT CAAATAGAAT GTGGTAATTT TTCAGACTTT ATGATCTGTT TCCAAAATTG	2100
GCACAAAGTG CTAGGGTTTA TATACACTTA TCGTAACGT ATTTTGTGTC CTGTGTTTTA	2160
TCATGTCAAT GCACTGTACT CTGTAAAAGT TTTGCAGACA AAATAGAAAG TATGATAATC	2220
CGTCAGAAGT ATGATGTAAA ACTGGAATCC TCTGTATTTT TTAAATGTTC TAAAAATTTT	2280
ATCGCTGTTA AGGTATTAAT CATTCAATAT TACTAATGGA ATAGAAATTC ATACTTTTGT	2340
ATGGACAACA AATTGATATT GCATTTATAG CACTGTAAGA AACTTTCATC TTGAGCAACT	2400
TTGTAGATGA TGGGTGTTTT ATTTTCAATC GCCATATTTG ATCAGTCATT GAAAATTGGC	2460
CCCACTGCTG TTTGTTTCAT TCTGTATGTA AAAACTGACA GTGAGACACA ACTTCTGAA	2520
CTGTGAGGGT GTCCCAAGGA AAGAAAAAC AGGAATACTT TAACAATTAA AAGAAAAAA	2580
ATGTTTTTTT TTTGCAAGG ACTCAGGAAA ATAAAAAGCA TTTTCTATTT TTAGACAAA	2640
TCACAAATGA AGTGTCTAAC TGCTATTAC TGTTTACCCA TATAAATAT GCTGCTAAAG	2700
TACATATTTT GCTGTCAATG GCTTGACAAT TTTTTTTTTC AAATTGAGAC ATGAGAGGTT	2760
ATATAGGGAC TATATTATCC AACACATATT TTCTTATTTT GCCACAAATT TCCACTTAAC	2820
AAATAAAAAA AGGCGAATGC TGTTTGGCAA AAAAAAAA	2859

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 368 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

1997-1998

90

Leu Ser Gln Met Ser Ala Arg Leu Asp Lys Ile Glu Glu Gly Gln Lys  
 275 280 285  
 Lys Thr Phe Asp Gly Gln Arg Thr Arg Gln Glu Glu Glu Lys Met His  
 290 295 300  
 Gly Arg Ile Thr Lys Leu Glu Leu Gln Met Asn Gln Asn Ile Lys Glu  
 305 310 315 320  
 Met Lys Ala Glu Val Asn Ala Gly Phe Thr Ala Val Tyr Glu Ser Ile  
 325 330 335  
 Gly Ser Leu Arg Gln Val Leu Glu Ala Lys Met Lys Leu Asp Arg Asp  
 340 345 350  
 Gln Leu Gln Lys Gln Ile Gln Leu Met Gln Lys Pro Glu Thr Pro Met  
 355 360 365

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 933 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TGCTTCGGAG ACCGTAAGGA TATTGATGAC CATGAGATCC CTGCTCAGAA CCCCTTTCCT	60
GTGTGGCCTG CTCGGGCCT TTTGTGCCCC AGGCGCCAGG GCTGAGGAGC CTGCAGCCAG	120
CTTCTCCCAA CCCGGCAGCA TGGGCCTGGA TAAGAACACA GTGCACGACC AAGAGTACGT	180
ATTCAGCCCG GGCCTGGTC CAGTGGCCTC CCCATCATCT GCAGCTGAGC CAGCGCAAG	240
GGCATGCTCA GTCCTCCTTT CCTTCTTCCT GTTCTATGG CTCCTTGACA TTCTCAAGG	300
ATGATTCTTA TTCCTTATG CCACCTATAA GTCAGGTATT CTTTTTCAT CATTGTATCA	360
CAGTGGAAG ATCTTTAGCG CCAATGGGG CACATTACTT GTCTGAATCC GGTCTCTCCT	420
TTTTTTCACC ACAGACAGAC ACACACACAT ACAAATAGAC ACACAGGTAC ACATACACAG	480
TCATAGTAGC AGAATCCAGA AAATAGCTAA GGTTCCTTGA CTATAACAAG ACCTTTTTTTA	540
AATCAACACA TTCAAACATT GAATCATTIG TTGCAGCTTT TGTCTGGGC CAGTTAGCCT	600
CACGCATTAT ACTCGTTTAT CCTTTGTTTT TAAGGCTGGG TGCAGTGGCT CACACCTGTA	660
ATCCAGTGC TTTGGGAGGC TGAGGCAGGT GGATTACTTG AGCCCAGGAA TTCGAGACCA	720

GCCTAGGCAA TATAGGGAAA ACCTGTCTCT AYTAATAAAT TGCAAAAAAT TAGCTGGATG 780  
 TGGCAGTACA TGCCTATGGT CCCAGCTACT TGGGGGGCTG AAGTGGGAGA ATCAAMTGAG 840  
 CTTGGGAAGT TGAGGGCTACA ATGAGCCAAG ATCACGCTCC TGCACTCCAG CCTGGGTGGC 900  
 AGAGTGAGAC CCTGTCTCAA AAAAAAAAAA AAA 933

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 92 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Met	Thr	Met	Arg	Ser	Leu	Leu	Arg	Thr	Pro	Phe	Leu	Cys	Gly	Leu	Leu
1					5				10					15	
Trp	Ala	Phe	Cys	Ala	Pro	Gly	Ala	Arg	Ala	Glu	Glu	Pro	Ala	Ala	Ser
			20					25					30		
Phe	Ser	Gln	Pro	Gly	Ser	Met	Gly	Leu	Asp	Lys	Asn	Thr	Val	His	Asp
		35					40					45			
Gln	Glu	Tyr	Val	Phe	Ser	Pro	Gly	Cys	Gly	Pro	Val	Ala	Ser	Pro	Ser
	50				55					60					
Ser	Ala	Ala	Glu	Pro	Ala	Ala	Arg	Ala	Cys	Ser	Val	Leu	Leu	Ser	Phe
65				70					75					80	
Phe	Leu	Phe	Leu	Trp	Leu	Leu	Asp	Ile	Leu	Gln	Gly				
			85					90							

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2956 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

CTGGTGTGGT	GGTTTAAAGT	TGTATATCAT	AGGGTCAGGT	GGCCTGGGTT	CATTCCCCAG	60
CTACGTAACC	TTTCTATGCC	TGAGTTTCCT	CATCTATAAA	ACAAGGATAA	TAATAGTGTG	120
TACTTCTTAG	GATTGTTTGT	GAGACTCATA	AATGAGAAAT	ACGTGAAAAA	CTCCCTCAAG	180
GCAGTGCTTG	ACACATAATG	AGCACTCAGT	TATCATGGTC	ATCATGGTCA	TCATCACTGC	240
TACCACCCT	GCTGCTGCTA	TTACCACCTCT	ACCTCTTCCC	CCTGAAACCT	TAATCACTTA	300
CCCTAGAAAC	AGTTAAATTA	CACTTCAGTG	GGAAGGATCT	CAGATTTCCT	AATGGCACCT	360
GCATTTATAT	AATGTTGATA	TTGCACGTTT	CTAGAAAAAC	TATCAAGAAG	AAACCAAAAT	420
GTGTTTCTGT	ACTTTGTAAA	CCTGTACAAT	AGTTAGAGAT	TAGAGGACCT	TTATAATCTA	480
CTACTAATTA	CTGTGAAAGT	AAACATTGTT	TAATATACCA	GTTCTTAAAG	AAATATTTTG	540
TCTAGTCATT	AATATTCTAG	TTCATCTCAA	AGCTTCCATT	TGACAATTTA	AAATTACTTA	600
AATTTTAATA	TTAAAGGAAA	CAGTTTTCCT	GATTCTCATG	AAAGTTCCTA	TTTGCACTGA	660
AGATGACTAA	ACCTTTTAGT	CATAGTTTTA	GAAGAATTGG	CTTTTTTATA	GCCATTTTAT	720
TTACATATGG	GTACTGCATA	GCAAAGGCAG	CAGATTAGCC	CTGTTTGTTT	TGCAGGGATG	780
AAAGGTAGCA	TTCCAGGAGA	TTAAGTTGTT	CTTGCTATTC	CCATTCTCTG	CTACATTTGC	840
CTACATTCTT	TGGTCCTTTC	TATTATTGTT	TTCTTTGGTG	GAATCCGCTT	GTGCTTTATG	900
GCTGGATATT	GTTATTTCAGC	AGATGAATCA	CAAGTTTAGC	CTGAGGGCCC	TAAAGCATCA	960
GAAATAAAAT	AGAGCCGAGC	AAAGTTTAAC	TTCTCTGGAA	CTTGCACTTT	TAGTTTCCAT	1020
GTATTTCTGG	AACCAAGATA	TTTCAAAGGC	TTACTTTATT	TCAGACACCT	ATTATCTTCA	1080
AGTCACAGAT	AACATATGAT	TCTGTAAAGT	GTTTCAAAGA	TTTTTGTTCA	CTAGACATTT	1140
TTAAATTTGT	TCAACTCCTC	CTCATCATTT	TAGAAATTAT	TTCTGTTAGG	TAAATTTAAA	1200
ACTAACAAATG	TATTTTAGTT	TATTTTCTTA	ATGATACCAG	TCACCTTTCT	GGGCTAACTA	1260
AACATTTTGT	GCAGCATTCT	CTTAGTTTAC	ATCCCTCCTT	CTTTCAGTCT	TCCTGTTTAT	1320
TAAGGCTGTC	CTGTAGCAAA	CAAAAGAGTG	ACTCATGTTA	AAAGTATTTT	AACTGCTCTA	1380
ATATATCTGA	GGAAGAATAA	CTTTCTAAAT	TAAAGTAATG	TATTTTATTA	AAATATTAATA	1440
TGCATTTTTT	GGCTATTCAT	TTCTGTATGT	AAAAAGAAAG	TTAACTTTAT	GGTGTATATG	1500
AAAATATGCT	AAATTTAGAT	TTTAGAGCAA	TATATAGGGA	GATATGTCAC	AAATTTCTAC	1560
ATTTTGGTTA	AATTATTAGT	ATTTTTTAT	ATTCAAATGT	GCCTTGATAT	TTAAATAATA	1620
TACTGAATGC	AGAATTTATG	TTATGTGAAC	CATTATGGAA	AATGTTAATG	TTAACAAAAAT	1680
GAGGTGTATT	GACTTTTCAA	CAATGTAAAT	TAAAGATGGT	ACATCTACTG	TTTAAAGGGCA	1740

GAGGAATTAA AAGAGTATAG ATACTGAAAT GTATCACTTA CTAGTAGTGT GGCTATAATC 1800  
 AAATTAATTA ATCTCTCTCT AGGCTTTAGC TTCTCATCT TAGTTTGTTT AGGCTACTGT 1860  
 AACAAAATAA CATAGATTAT GTACTTTTAA ATGACAGAAG TTTATTCGGC ATGGTTTGGG 1920  
 AGACTAGGAA GTCTAAGATT AAAGAACCAG CAAATTGGT GTCTGATGAG GACCCATTCC 1980  
 TTTGTTTACA GATGATGCCT TCTCATTGTG TTTTCAAATG TTGAAGGAG CTAGCTAGCT 2040  
 TTCTGGGGTC TCTTTGTAA AGGCACTAAT CCCAGTCATT AGGGCAAATT GGCTCCTACA 2100  
 GGCCCCACCT ATCTCCTAAT ACCATCACCT TGAGGATTAA GATTCTTACA TATGAATGAA 2160  
 GCAGGTGTG TAGAAGGTCA GTCAGTTAGA CCATAGCACC ATCTGTAAAA TTGAATAGTA 2220  
 ATTTACTGCC TCATTGGATG TCAGGATTAA AGGAGATAAG ATTTTATTAG TTACTAGTTA 2280  
 CCATAGTGGT TTTTTTTTTA CACTATAATG TTCGTTTTTT TGTTCATGC TTGTACCTTC 2340  
 AACATTTCT TCCATTGAA TACTTCTTT GTCTCTGTA GGCTGTCTG TCCACTTAGG 2400  
 TGTAAGATGT GTTTTGTGT CAGGAATGAT GGTGCAATGC TAATGTTCCA TTGCCCTATT 2460  
 TGGCAATACT CTGATCATTA ACTATAAAGA ATAACCAGG TGTTAACTAA CTCTCCTTGC 2520  
 CTGACAGTAG TGCTGCCACT ATTCCTTGT TCTGTGTTAA TAGATGAGGT TTGTATGGTC 2580  
 CTGTTATTCC AGCCTCCAGA CACCATTCCA GATCAACTGG TGCCYTCWAC GCCCCCGAAG 2640  
 TGTATGGGGC CTCAGGTGAA GGATGAGWAC ATTTTCACTA TCATCTGGCA TTCACTCTCAG 2700  
 ATTTTATCCT TTTCAGTTTC CATTAAATAA TATTGATGTT TTTAAATTGA TTTTTATTA 2760  
 TTAAATTTA ATTGTTGGA GAATAAACTT TTTTTTTCT TTCTCCCAA GTAACGTTT 2820  
 CCCCTTTAGC AACTGTATTG AGCATTTTTC TCACTGGTAT ATGGACATTT TTTGTATATA 2880  
 CCTGTTGTGT CATTTTTAAA TATAGAATTG TTTTATGTT CTCATCTTGT TATATATGTT 2940  
 TAAAAAATAA AAAAAA 2956

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Met	Thr	Lys	Pro	Phe	Ser	His	Ser	Phe	Arg	Arg	Ile	Gly	Phe	Phe	Ile
1				5				10					15		
Ala	Ile	Leu	Phe	Thr	Tyr	Gly	Tyr	Cys	Ile	Ala	Lys	Ala	Ala	Asp	
			20					25					30		

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1325 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

AATCGGGAAA	AAAAGCCATG	TATTCCTTCG	TTTCTCTCTA	AAAGAAGAAA	AATATAATTT	60
AAAATACAT	TGCGTATTTT	CTAAAAAAT	AAATTTATAG	TGTTAATATT	CATAGGGTCA	120
ATCAAAATGA	AGCTTCTCCT	TTGGGCCTGC	ATTGTATGTG	TTGCTTTTGC	AAGGAAGAGA	180
CGGTTCCTTC	TCAATGGTGA	GGATGACAAT	GACGATGGTG	ACCCACTTCA	TCCATCTCTG	240
AATATTCCTT	ATGGCATACG	GAATTTACCA	CCTCCTCTTT	ATTATCGCCC	AGTGAATACA	300
GTCCCCAGTT	ACCCTGGGAA	TACTTACACT	GACACAGGGT	TACCTTCGTA	TCCCTGGATT	360
CTAACTTCTC	CTGGATTCCC	CTATGTCTAT	CACATCCGTG	GTTTTCCCTT	AGCTACTCAG	420
TTGAATGTTT	CTCCTCTCCC	TCCTAGGGGT	TTCCCGTTTG	TCCCTCCTTC	AAGGTTTTTT	480
TCAGCAGCTG	CAGCACCCGC	TGCCCCACCT	ATTGCAGCTG	AGCCTGCTGC	AGCTGCACCT	540
CTTACATCCA	CACCTGTAGC	ATCTGAGCCT	GCTGCAGGGG	CCCCTGTTCG	AGCTGAGCCT	600
GCTGCAGAGG	CACCTGTTGG	AGCTGAGCCT	GCTGCAGAGG	CACCTGTTCG	AGCTGAGCCT	660
GCTGCAGAGG	CACCTGTTGG	AGTGGAGCCA	GCTGCAGAGG	AACCTTCACC	AGCTGAGCCT	720
GCTACAGCCA	AGCCTGCTCT	CCCAGAACCT	CACCCCTCTC	CCTCTCTTGA	ACAGGCAAAAT	780
CAGTGAAATT	CTCTAGAAGA	GTACCATGGG	TTCATTTCTA	TACTGATGCA	GAAATAAGTG	840
AAATCTACAA	AAGTTTTCTT	TCTTTTCCAA	AGACTATTTC	ATTCTGTAGT	ATTGAGAGTA	900
TTTATCTCAC	TACATGATT	TGTTTGTGGT	AGTTATTTC	TTGACTTAA	TTTATATTGA	960
AAAAACATTG	ATAATTAAAT	AAATAAAATA	GATAATTTAG	ACCAATGGTG	ATAAGGTCTG	1020
GATGAAAAC	ACGCTATGGA	GGACTGAAAT	GGCAATCATT	CAGCCTAGCC	TGGAGTCTGA	1080

TTATACAGCT ACTATAGGAT GATGTTAGTA TTGGTTTGA GTGCAATAGG TTTTTCCTA	1140
AACAAACATA TTTTGTAGTC AATGAACTTT TTGTCACAAA ACAGTAAAC ATCTGTGTTT	1200
AACCTATGGT AAACAACATG TTAATGAACT ATGCTATCCA TGACTTAATG GACAGTTCAA	1260
AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	1320
AAAAA	1325

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Met	Lys	Leu	Leu	Leu	Trp	Ala	Cys	Ile	Val	Cys	Val	Ala	Phe	Ala	Arg	1	5	10	15
Lys	Arg	Arg	Phe	Pro	Phe	Ile	Gly	Glu	Asp	Asp	Asn	Asp	Asp	Gly	His	20	25	30	
Pro	Leu	His	Pro	Ser	Leu	Asn	Ile	Pro	Tyr	Gly	Ile	Arg	Asn	Leu	Pro	35	40	45	
Pro	Pro	Leu	Tyr	Tyr	Arg	Pro	Val	Asn	Thr	Val	Pro	Ser	Tyr	Pro	Gly	50	55	60	
Asn	Thr	Tyr	Thr	Asp	Thr	Gly	Leu	Pro	Ser	Tyr	Pro	Trp	Ile	Leu	Thr	65	70	75	80
Ser	Pro	Gly	Phe	Pro	Tyr	Val	Tyr	His	Ile	Arg	Gly	Phe	Pro	Leu	Ala	85	90	95	
Thr	Gln	Leu	Asn	Val	Pro	Pro	Leu	Pro	Pro	Arg	Gly	Phe	Pro	Phe	Val	100	105	110	
Pro	Pro	Ser	Arg	Phe	Phe	Ser	Ala	Ala	Ala	Ala	Pro	Ala	Ala	Pro	Pro	115	120	125	
Ile	Ala	Ala	Glu	Pro	Ala	Ala	Ala	Ala	Pro	Leu	Thr	Ser	Thr	Pro	Val	130	135	140	
Ala	Ser	Glu	Pro	Ala	Ala	Gly	Ala	Pro	Val	Ala	Ala	Glu	Pro	Ala	Ala	145	150	155	160
Glu	Ala	Pro	Val	Gly	Ala	Glu	Pro	Ala	Ala	Glu	Ala	Pro	Val	Ala	Ala				



	165						170						175										
Glu Pro Ala	Ala Glu	Ala Pro	Val Gly	Val Glu	Pro Ala	Ala Glu	Glu Val	Pro Ala	Ala Glu	Glu Val	Pro Ala	Ala Glu	Glu Val	Pro Ala	Ala Glu								
						180						185						190					
Pro Ser Pro	Ala Glu	Pro Ala	Thr Ala	Lys Pro	Ala Glu	Pro Ala	Ala Glu	Pro Ala	Ala Glu	Pro Ala	Ala Glu	Pro Ala	Ala Glu	Pro Ala	Ala Glu								
						195						200						205					
His Pro Ser	Pro Ser	Leu Glu	Gln Ala	Asn Gln																			
210						215																	

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 533 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

CGGGGCAGGC AGGCTGTCGG GGTACAGAGC TGGGATCTGG GAAGGAACAG AGAGGGCCGC 300  
 TCAGGGAGAG GAAGCACAGT GCCACCGSAG GCACGCACTC AGCAGGCACT CGCAGGCTGG 360  
 GCAGAGGTAG AGAAGCAGCG CTGCACAGGC AGGCAGTGTA CCCAGGGCTC TTAGAGCCGG 420  
 GCAGGAGAGC TGGTGTGGGA CCTGGGAGGA GGACAGGAGC CTTCAAAGCA GCACCGCCTG 480  
 ATTGCAGCCA GGAGGGTAGC ATCAAGGAAG ATGGAATGCT GGCCAGGCCA CAT 533

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 101 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Met Ser Ser Thr Gly Gln Ala Gly Cys Arg Gly Thr Glu Leu Gly Ser  
 1 5 10 15  
 Gly Lys Glu Gln Arg Gly Pro Leu Arg Glu Arg Lys His Ser Ala Thr  
 20 25 30  
 Gly Gly Thr His Ser Ala Gly Thr Arg Arg Leu Gly Arg Gly Arg Glu  
 35 40 45  
 Ala Ala Leu His Arg Gln Ala Ala Asp Pro Gly Leu Leu Glu Pro Gly  
 50 55 60  
 Arg Arg Ala Gly Val Gly Pro Gly Arg Arg Thr Gly Ala Phe Lys Ala  
 65 70 75 80  
 Ala Pro Pro Asp Cys Ser Gln Glu Gly Ser Ile Lys Glu Asp Gly Thr  
 85 90 95  
 Ala Ala Arg Pro His  
 100

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 458 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

TAGGCAGTCA TCTTTGTAAA CCTCCACTGG TGCTGGCTGC GTTTAGAACA TACTCCATAT	60
AAAAACAGGCC CTGGGATTAC AGGCATGAGC TACCGTGCCT GGCCCCCTTT TTTTAAATTA	120
CAGAGAAATA AGTTACACCT TAGTATCAGA TATTAATTTT CTTCAGTGTT CAGGCAATTA	180
GTATTTAGAA AGCTCTTGTC ATGAGATGGC TCTGGGATGT GATGATGATT GTTGGGATTG	240
AAAAAATGGT AGTATCATGG AGAGATCATA ATAAATCTTT AGTATTAATA GTGGTTTTCG	300
TTTCAGTTAG GGAGAAAAAT TAGATTGTAC TATTTTTCCT CTATGATTTC CTTCAGTTAT	360
CTTCCAAATG TTGTTTTTTC CCCACAGCCC CCTTAACATT GTTCTCTATG CACTTCTCAA	420
TACATTTTCA TTTGTTTCTC AAAAAAAAAA AAAAAAAA	458

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

TTTTTTTTTT TTTTGTAGA GACAGGGTCT TGCCATTTTG CCCAGGTTGG TCTCAAACCT	60
CTGAGCTCAG GCTATCTGCC CACCTTGGCC TCCCAAAGTG CTGGGATTAC AGGTGTGAGC	120
CACTGTGCCC GGCCTGTATT GTTTTAAGTT ACACTTATTC CTTTAAATAT TCAGAAATTTG	180
TTAAGCATTT AAAACAAATT CATAAATTAA AACCTCCTTG AGATACCATT TACCATGTAG	240
TTTGATGAAC ATAATACATG GTGCATTACA TTGGCAAAG CAGTGGGGAA AAAGATGCTT	300
TTATAAATGT CTGTGGGAG TTAATTTGTG TAACTTCTAT TAACTTTTG TAATAGCTAC	360
CAAAATATGT TATTCTATC TACCTCTCTC TCTCTGACTC AACAGTTCCA TTTCTAGGTT	420
TTGTGTTGTG GATATTCTTG AACATTGTGA AATGTATACA GGGAGGCTTC ACAGCAGCAC	480
TGTTTGTTTC AAATGATTTG AAAACAACCT CTCCATAAAC GAGATAGGCT AAATCAAGCA	540
TGGCACACCT ATACAATGGA TGCGGCCATT AAAAAGAACA AGGCAGCTCA TATGCATCAA	600
TATAAAAAGG TCTATAAATC ATACTATCAA ATGAAAATAG CAAGATGCTA CCATTTATAT	660
TAAAAGAGG ACAAAATATT AATATATTCA TGGTTGCTTG TCTATGTGGA ATATTTCTGG	720

ATATATACAT AAGAAGTTAC ATTGTTTACC TATGGGCAGG TTACTACTGG GTGGCTTGTG 780  
 GGTGAGGSCA GGAAGAGCTT ACTTTCCATG GTAAACCTTT TTGTATATTT TGCAGCATTC 840  
 AAAAATTCTA ATTTAAAGTT TATTTTAGAA AAATGCCCCC ATGTATACAA GTGATTTCCTA 900  
 AGTTCCTCCT TCAATATTTT TAATGATTAT GGAACACACT GAACCTCTTT TTTATTATTC 960  
 TAGCTGTGAA CTCTGTCTGC TGTCTACATG CACATATATA ATCTATGTAA TATTIAAATT 1020  
 TATATCCTTT ATATGTCAGT TGGGTGGTGA GTAAAGAAA AATATATTTT TATCAGCAAA 1080  
 CTTGGTAAAT TGTTGAGGTT TCTGATATAG TCAGAGGTAG TTGCTTATCA CAACATTAGG 1140  
 TAAGTTTTTA AARACACCTA TTTAAACAC ACTGATGTAT ATATATATTG GTCTGTTTTT 1200  
 ATGCTGCTGA TAAAGACATA TCCAAGACTG GGAAGAAAAA GAGGTTTAAT TGGGCTTATA 1260  
 GTTCCACATG GCTGGGGAGG CCTCAGAATC ATTGCGGGAG GCAAAGGCA CTCTCTACAT 1320  
 GGCAGTGGCA AGAGAAAAAA AAAAAAAAAA 1350

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 46 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Met	Leu	Pro	Phe	Ile	Leu	Lys	Arg	Gly	Gln	Asn	Ile	Asn	Ile	Phe	Met
1				5				10						15	
Val	Ala	Cys	Leu	Cys	Gly	Ile	Phe	Leu	Asp	Ile	Tyr	Ile	Arg	Ser	Tyr
			20					25					30		
Ile	Gly	Tyr	Leu	Trp	Ala	Gly	Tyr	Trp	Val	Ala	Cys	Gly			
			35				40					45			

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1598 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

TCGGGACACT ACATGAAGTC CTGAAAATAA CAGAGAAACT GTTATATCTT TTTAATGATT	60
TATTTGCAAG TATTGAGGTT GACCTGAAAA ACAATGAAAC ACATGAACAC ACTTCCGATT	120
TTCTCCTCGC TGATTAGCTT CCTGCCTGCT GTCAGTGCTG GACGAAGTGC TATAACTACT	180
TTATGTAACA TTACAGAACA GCTAGAGGTC CTGGGGTAAG AGAAAAAAG CACATCACAA	240
CAAAATGTGAA AGCCTTCATT ATTACACGTT CCAGTTTGTC TCGCTGTGTA GGCATAAGCT	300
AATGGTTTAT TTTCAGAAAG CTGCCTGAAA CGTTGCTTTG TATTCTTCTA GGAAGAAGCT	360
TAATTCCCTCC TGAGGAAGTC TACTTTCTGA GCCAACTGC TAATTTTCTG CGGAAGTGC	420
TAGAAGATCA TTCAAGAGAC CTGCAGTTG CACTTCTCG TAAAAGTTAA AAAAAAAAAA	480
AAAAAAAAAG GTTTTCCCG GCCTTTGAAC ATTTTGCTTA TGAGAGTTT GCATATATTT	540
TATACTTGAG TAGACAACCT TAATAATCCA TATTATACT ATCGCAGAAG TAAGCATTG	600
GCAAACGTTT AGCCATTAGC ACTCATTTAA CCTGTGTAGC AATATTCITT TGAAAAAAGT	660
GCCAGTCTTT ATGTGATAAA CTAAGAAGCC CATTGAATAT AAAANTGTGT NGGACTGAAA	720
CNGTGACCTT ATATTATTGC TAAGGGAATA TGAGATTAA TCCTACAGG GGCCANAACC	780
ANANAAAGGC TTCCAGCAAC TTCGATNAAA NTANTTTGGC CACATNTCAA GCCAATTGTT	840
TGTACTATTT ATGTACCTTT TTCATACTG GAATTGCCAA ATAAGCATGG AGATCTAAAT	900
GRAAAAAAAA AAAAAAAAAA AAAGCGGCCG CAGGTCTAGA ATTCAATCGG AAAAAACAAA	960
GAGAAGAAAC ATACTGCCCC ATCTTGTTTG CATGAACTC TAGAATCTGG TGTTCCTCTA	1020
TTTATCTGCT CCTCTTTGCT CTACCTTGGN ATTTCTTTTT TTTTTCITT GTAACATAGG	1080
TTTTTACCTA AAGTTTAAAC TTTTATTAT TATTTCTCT CTAAATCTT GCTAGTTAAT	1140
AACATTATTA ACTTCAAGAT TTTAGAAGAG CAGTGATGAT AGTAATGATC GATAACTAGA	1200
CTATCGAGTT TCAGAAGAAA CTCCAAGTA TATATAATGT TTGACATAGC CTTTATTCT	1260
ACAAATCTAC TACCTGTAAA CTAACATTTT AAAATACCTG TATATGGCTG GGTGTGGTGS	1320
CTTACACCTG TAATCCCAGC AGTTTGGGAG CCTGAGGTGG GCAGATTGCT TGAGCCCAGG	1380
AGTTGGAGAC AAGCCTGGAC AAAATAGACC TCTCTTACA AAAAGTACAA AAAATTGGCT	1440
GGGTGTGGTG GCACACGCCT GTGGTCCCAG CTACTCGGGA GGCTGAGGTG GGAGGATTGC	1500
CTGAGCCCGG GAGATGGTGG TTGCAGTGAG CTGAGATCAC CCCATTGCAC TCCAGCCTGS	1560
ATAACAGAAT AAGATGCTGT CTTAAAAAAA AAAAAAAA	1598

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 41 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Met Lys His Met Asn Thr Leu Pro Ile Phe Ser Ser Leu Ile Ser Phe  
1 5 10 15  
Leu Pro Ala Val Ser Ala Gly Arg Ser Ala Ile Thr Thr Leu Cys Asn  
20 25 30  
Ile Thr Glu Gln Leu Glu Val Leu Gly  
35 40

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1257 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

CATGGCGTCC AGGTCTAAGC GGCCTGCCGT GGAAAGTGGG GTTCCGCAGC CGCCGGATCC 60  
CCAGTCCAG CGCGACGAGG AAGAGGAAAA AGAAGTCGAA AATGAGGATG AAGACGATGA 120  
TGACAGTGAC AAGGAAAAGG ATGAAGAGGA CGAGGTCATT GACGAGGAAG TGAATATTGA 180  
ATTTGAAGCT TATTCCTAT CAGATAATGA TTATGACGGA ATTAAGAAAT TACTGCAGCA 240  
GCTTTTCTA AAGGCTCCTG TGAACACTGC AGAATAACA GATCTCTTAA TTCAACAGAA 300  
CCATATTGGG AGTGTGATTA AGCAAACGGA TGTTTCAGAA GACAGCAATG ATGATATGGA 360  
TGAAGATGAG GTTTTGTGTT TCATAAGCCT TTTAAATTTA ACTGAAAGAA AGGGTACCCA 420  
GTGTGTTGAA CAAATTCAAG AGTTGGTMT ACGCTTCTGT GAGAAGAACT GTGAAAAGAG 480  
CATGGITGAA CAGCTGGACA AGTTTTTAAA TGACACCACC AAGCCTGTGG GCCTTCTCCT 540

AAGTGAAAGA TTCATTAATG TCCCTCCACA GATCGCTCTG CCCATGTACC AGCAGCTTCA 600  
 GAAAGAACTG KCGGGGGCAC ACAGAACCAA TAAGCCATGT GGGAAAGTGCT ACTTTTACCT 660  
 TCTGATTAGT AAGACATTGT TGGAAGCAGG AAAAAACAAT TCCAAAAAGA AACCTAGCAA 720  
 CAAAAAGAAA GCTGCGTTAA TGTTTGCAAA TGCAGAGGAA GAATTTTCTT ATGAGAAGGC 780  
 AATTCTCAAG TTCAACTACT CAGTGCAGGA GGAGAGCGAC ACTTGTCTGG GAGGCAAAATG 840  
 GTCITTTGAT GACGTACCAA TGACGCCCTT GCGAACTGTG ATGTTAATTC CAGGCGACAA 900  
 GATGAACGAA ATCATGGATA AACTGAAAGA ATATCTATCT GTCTAACCCA TTTCCAATGG 960  
 ACAGTGATGG GCTTGTGTTT GTAAAAATAC CAGAAAACCT AGTGGAGATT TACTGAAAAA 1020  
 CTCAGACTTT ATTCAGATTA AGTTCCTCTA CAAAAAGTAG GGTTCGTGCC CATGTGTYTC 1080  
 TGACACATTT ACAAATAC AGTTTTTTAA AATTTTGGTC AAATTATGAG TGGTTGATTT 1140  
 AAAAAGTTTT CCAAGAAGAA GAAAAGCATG GAGTAGTAAT TTAAAGAACT CAATAAAAAA 1200  
 TTCTATTTTT TATTTAAAAA TAATAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAA 1257  
 (2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 314 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Met	Ala	Ser	Arg	Ser	Lys	Arg	Arg	Ala	Val	Glu	Ser	Gly	Val	Pro	Gln
1				5					10					15	
Pro	Pro	Asp	Pro	Pro	Val	Gln	Arg	Asp	Glu	Glu	Glu	Glu	Lys	Glu	Val
			20					25					30		
Glu	Asn	Glu	Asp	Glu	Asp	Asp	Asp	Asp	Ser	Asp	Lys	Glu	Lys	Asp	Glu
			35					40				45			
Glu	Asp	Glu	Val	Ile	Asp	Glu	Glu	Val	Asn	Ile	Glu	Phe	Glu	Ala	Tyr
			50			55					60				
Ser	Leu	Ser	Asp	Asn	Asp	Tyr	Asp	Gly	Ile	Lys	Lys	Leu	Leu	Gln	Gln
	65					70				75				80	
Leu	Phe	Leu	Lys	Ala	Pro	Val	Asn	Thr	Ala	Glu	Leu	Thr	Asp	Leu	Leu
				85					90					95	

Ile	Gln	Gln	Asn	His	Ile	Gly	Ser	Val	Ile	Lys	Gln	Thr	Asp	Val	Ser	
			100					105					110			
Glu	Asp	Ser	Asn	Asp	Asp	Met	Asp	Glu	Asp	Glu	Val	Phe	Gly	Phe	Ile	
	115					120					125					
Ser	Leu	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Gly	Thr	Gln	Cys	Val	Glu	Gln	
	130				135						140					
Ile	Gln	Glu	Leu	Val	Xaa	Arg	Phe	Cys	Glu	Lys	Asn	Cys	Glu	Lys	Ser	
145				150					155						160	
Met	Val	Glu	Gln	Leu	Asp	Lys	Phe	Leu	Asn	Asp	Thr	Thr	Lys	Pro	Val	
			165					170					175			
Gly	Leu	Leu	Leu	Ser	Glu	Arg	Phe	Ile	Asn	Val	Pro	Pro	Gln	Ile	Ala	
	180						185						190			
Leu	Pro	Met	Tyr	Gln	Gln	Leu	Gln	Lys	Glu	Leu	Xaa	Gly	Ala	His	Arg	
	195					200						205				
Thr	Asn	Lys	Pro	Cys	Gly	Lys	Cys	Tyr	Phe	Tyr	Leu	Leu	Ile	Ser	Lys	
	210					215					220					
Thr	Phe	Val	Glu	Ala	Gly	Lys	Asn	Asn	Ser	Lys	Lys	Lys	Pro	Ser	Asn	
225				230					235						240	
Lys	Lys	Lys	Ala	Ala	Leu	Met	Phe	Ala	Asn	Ala	Glu	Glu	Glu	Phe	Phe	
			245				250						255			
Tyr	Glu	Lys	Ala	Ile	Leu	Lys	Phe	Asn	Tyr	Ser	Val	Gln	Glu	Glu	Ser	
	260						265						270			
Asp	Thr	Cys	Leu	Gly	Gly	Lys	Trp	Ser	Phe	Asp	Asp	Val	Pro	Met	Thr	
	275						280					285				
Pro	Leu	Arg	Thr	Val	Met	Leu	Ile	Pro	Gly	Asp	Lys	Met	Asn	Glu	Ile	
	290					295					300					
Met	Asp	Lys	Leu	Lys	Glu	Tyr	Leu	Ser	Val							
305					310											

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1544 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:



CGCGTCTGTC CACACAAGCT GGGCGGCGGA GGGCACGCAG CCGGGCCTTC TTCTCTCTGG	60
GACCCCTCCGC CAGCGCATAG CCGCAGGCCG GTGTGACTTC TGACCCCTCG GTTCTGAGGG	120
TACGGTGACC CCTAGTGGGC AGTTTGCAA ATGTGATTCC TTCTTCCCAA CTCCTCATCC	180
CCCTTCCCT TCCCGTCACG TCCTGTTTGG GGGTTAATTC GGTTTTTTCT CTGTGTCATC	240
GCGCCTACTG TGCCTGTGCG ATACGCTGTG TGGGGGTGAG AGTTTGTITT CTGGAATGGT	300
AGGTGCTGGG AGGAGGAGTT TGATGGAGGG CTTCCTGGCT GCTTCTGGCC CTCACCTCGT	360
GGAGGCCCTC ACAGAGACCC TGTGGGCCCT GGCCCTGTGC TGGCACTGTG CCAGTCATGA	420
GGCAGCTCTG ATCACTTCCC CACTGTGGAA ACAGGACTGA CCCAGCCTTC AGTGTGGGCT	480
GCTGAAGCTA TCCTCCTCAG GCCTCAGGGA TGACCTCCTG CCTGAGCCTC TCACAGGCTG	540
GCTGTGGGCC AGTTTCATCT GCTTTCCTGT TGGGGTCCC GGGCCTCTGC TGTCTTGAC	600
CCACTGGTGT TCTGTGCAAG GCTTCTTCCC ATTCACCAAG TGACACACCT GCATCTGCCG	660
CTCGGCATGC ACCAGTTCCA CACACCATCC CATTTACAG ACAAGGACGC TGAGGCCCTG	720
AGCAGCAGTG TGACTTGCTC AAGTCCAGT GAGTGACCTC ATTCCCAGA AAAGGCTCCT	780
CCACACCCAG AGTACAGCCT GGGTAGGGGG AAAATCAGTT CTTTCAGCTA CCACCCATCC	840
AACCTTTGGG CCTATGTGAA AAGAAAGGAA CTAAGCTGGG TGTGTTCTGT CTGGACCTGG	900
GGAGGCCCTC GAAGGCAAGG AGGGAACTG TCCAGCTGT TCTGTCTTAG GGGAGGGGGA	960
CATAGCCCTA GCAGGAGCTC CCAGCCCCTC TTGGCACTCT GACACACAAG TACACCCATC	1020
TGGGGCCCGC TTTGCCACGA AGAGCTGGGC AGGCCTGCAG GGTGTGGGGA AGGAGGACAC	1080
AACCTCAAGA AAGGAAGCGT GAACCCAGG GAACAGCGGG TCCCTTCCTC CCTCAGACAC	1140
AAGCCACCTC AGCTTGTGGC TCTTGGCCCC CAGCCCACC AACCCACCTG TTCATTATT	1200
CAACAGACAA TGACAGCTGA TATTTATTGG ACATTGACAC CATGCCAAGC ATTGCGCTTG	1260
GATTATCCCA TTTGTTTCTC ACAGCCGCTA TTTATTGTCT GCTCCTCTGT GCCAGGTGCT	1320
GTGCTCTGGG CAGGGGCACT GCATGGGCTG CCTGCCTGG TGGAGCTTGT GGTCTGATGG	1380
GTGAGGCTGA CCCAAGCCCA CCCCATTGCC AACAGGCCA GGGCAAGAGT ACACACAGGG	1440
GCCTCATACC ATATGTCTAA ATATTTAAAA GTTATCAATC AAGCTAACAA CTGTTAAATA	1500
AAATATGTTC TATCTCTCTA CTTTGAAAAA AAAAAAAAAA AAAA	1544

(2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 72 amino acids
  - (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

```

Met Pro Ser Ile Arg Leu Gly Leu Ser His Leu Phe Leu Thr Ala Gly
 1           5           10           15

Ile Tyr Cys Leu Leu Leu Cys Ala Arg Cys Cys Ala Leu Gly Arg Gly
          20           25           30

Thr Ala Trp Ala Ala Cys Pro Gly Gly Ala Cys Gly Leu Met Gly Glu
 35           40           45

Ala Asp Pro Ser Pro Pro His Cys Gln Gln Gly Gln Gly Lys Ser Thr
 50           55           60

His Arg Gly Leu Ile Pro Tyr Val
 65           70

```

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

CNATGCAGGTC TAACTCCTCC ACTCTGGG

29

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

TNAGTTTGGTG CTCTGCTCTG ATATTGAC

29

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

GNCATCAATAT CCTTACGGTC TCCGAAGC

29

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GNAAATAGGAA CTTTCATGAG AATCAGGA

29

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

ANACAATGCAG GCCCAAAGGA GAAGCTTC

29

09746763.123100

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GNITGCTTGT CGCTTTCGCA CTTACGTT

29

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

ANTGGTAGCAT CTTGCTATT TCATTGA

29

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

TNGGAAGTGTG TTCATGTGT TCATTGTT

29

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GNCCCTCGTCCT CTTATCCTT TTCCTTGT

29

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

ANCACTGGCA CAGAGGAGCA GACAATAA

29

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2271 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

GGCGAGCCTT TGAGGGGAAC GACTTGTCGG AGCCCTAACC AGGGGTATCT CTGAGCCTGG 60  
TGGGATCCCC GGAGCGTCAC ATCACTTTC GATCACTTCA AAGTGTAAGG GGGGCCCTAC 120  
TGACCTCTGG AATTTAGGGG GGCCTACCTA GCGGCATCC ACACAGAGA GAATTCCCTT 180  
GGAGAGGGGA CCTGTGTCT CGGCTGTCCC TCTCATCCG GTAGAAAGTC CCTCATCTGG 240  
GGGCTCCCGA ACTCAGCCCT CTCACATTGT GGCCGGCTTT ACTGACCCTC ACAGACCCAG 300  
GCTGGGCCCT CCCGATAGAG GCCAGCCAAA GGTTCACCTA GCCTCTCTTT CAAGGCTGGT 360  
GTATCTCTAA ATCTTAGACC CTCCTCCGTT ACCGTCAGCC AGGTGGGATG CCCACGTTTT 420  
GGAGAGAAAC CGTTCTGAGG AACCCGGGCC TCTGGGTCCC AGCTGGCTCT CCGCCCCCA 480  
GGTTATGTAT TCTGGGTTGG CCACAAACAG TGGAATTCTA GGCACTCCCG GGACAGGGTG 540  
GGACTGTGCT CCTATTTCAT GCAACCAGCA AATATTACG GCACCTTGTG TGTGCCAGAC 600  
AGCAGACCGA GGACACGGTT GTTACCAAGA CCAGGCTGTT GCCTTGAAG AGCCAGAGAC 660

GTGTCAAGGG AGACAGCCAC ATCAGGCCAG AAATACATGA CAGCTGGATT AGCCCTGGGA 720  
 GAGGAGAGGCC CAGATGTGGG AGCTCAGGGG AGGTGCAGCT CAACGTGGAG TTTGGAGGAG 780  
 GCTACCTTTGA CTTTGTGAATG CCAAGTGGGA GCCAGCCAGA TGAAGGGGGT TAAAAACTAA 840  
 TATTTATATG ACAGAAGAAA AAGATGTCAT TCCGTAAAGT AAACATCATC ATCTTGGTCC 900  
 TGGCTGTTCG TCTCTTCTTA CTGGTTTTCG ACCATAACTT CCTCAGCTTG AGCAGITTTG 960  
 TAAGGAATGA GGTACAGAT TCAGGAATTG TAGGGCCTCA ACCTATAGAC TTTGTCCCAA 1020  
 ATGCTCTCCG ACATGCAGTA GATGGGAGAC AAGAGGAGAT TCCTGTGGCT ATCGCTGCAT 1080  
 CTGAAGACAG GCTTGGGGGG GCCATTGCAG CTATAAACAG CATTTCAGCAG AACACTCGCT 1140  
 CCAATGTGAT TTTCTACATT GTTACTCTCA ACAATACAGC AGACCATCTC CGTCTCTGGC 1200  
 TCAACAGTGA TTCCCTGAAA AGCATCAGAT ACAAATTGT CAATTTTGAC CCTAAACTTT 1260  
 TGGAAAGGAAA AGTAAAGGAG GATCCTGACC AGGGGGAAATC CATGAAACCT GTGATATTCT 1320  
 TGCCCTTTAC AATACAGCAC TGAAGCCAGG ACATGCAGCT GCATTTTCAG AAGATTGTGA 1380  
 TTCAGCCTCT ACTAAAGTTG TCATCCGTGG AGCAGGAAAC CAGTACAATT ACATTGGCTA 1440  
 TCTTGACTAT AAAAAGGAAA GAATTCGTAA GCTTTCCATG AAGCCAGCA CTTGCTCAT 1500  
 TAATCCTGGA GTTTTTGTTG CAAACCTGAC GGAATGGAAA CGACAGAATA TAACTAACA 1560  
 ACTGGAAAAA TGGATGAAAC TCAATGTAGA AGAGGGAGCTG TATAGCAGAA CCCTGGGTGG 1620  
 TAGCATCACA ACACCTCCTC TGCTTATCGT ATTTTATCAA CAGCACTCTA CCATCGATCC 1680  
 TATGTGGAAT GTCCGCACC TTGGTTCAG TGCTGGAAAA CGATATTTCAC CTCAGTTTGT 1740  
 AAAGGCTGCC AAGTTACTCC ATTGGAATGG ACATTTGAAAG CCATGGGGAA GGACTGCTTC 1800  
 ATATACTGAT GTTTGGGAAA AATGGTATAT TCCAGACCCA ACAGGCCAAT TCAACCTAAT 1860  
 CGGAAGATAT ACCGAGATCT CAAACATAAA GTGAAACAGA ATTTGAACCTG TAAGCAAGCA 1920  
 TTCTCAGGA AGTCTCGGAA GATAGCATGC GTGGGAAGTA ACAGTTGCTA GGCTTCAATG 1980  
 CCTATCGGTA GCAAGCCATG GAAAAAGATG TGTCAGCTAG GTAAAGATGA CAACCTGCCC 2040  
 TGCTGGCAG TCAGCTTCCC AGACAGACTA TAGACTATAA ATATGCTCCTC ATCTGCCTTA 2100  
 CCAAGTGTTT TCTTACTACA ATGCTGAATG ACTGGAAAGA AGAAGTATA TGGCTAGTTC 2160  
 AGCTAGCTGG TACAGATAAT TCAAACTGCT TGTGTGGTTT AATTTGTGTA CCGTGGCCCT 2220  
 GATCTGTAAA TAAAACTTAC ATTTTTCAT 2280

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Met Ser Phe Arg Lys Val Asn Ile Ile Ile Leu Val Leu Ala Val Ala  
 1 5 10 15  
 Leu Phe Leu Leu Val Leu His His Asn Phe Leu Ser Leu Ser Ser Leu  
 20 25 30  
 Leu Arg Asn Glu Val Thr Asp Ser Gly Ile Val Gly Pro Gln Pro Ile  
 35 40 45  
 Asp Phe Val Pro Asn Ala Leu Arg His Ala Val Asp Gly Arg Gln Glu  
 50 55 60  
 Glu Ile Pro Val Val Ile Ala Ala Ser Glu Asp Arg Leu Gly Gly Ala  
 65 70 75 80

Ile Ala Ala Ile Asn Ser Ile Gln His Asn Thr Arg Ser Asn Val Ile  
85 90 95

Phe Tyr Ile Val Thr Leu Asn Asn Thr Ala Asp His Leu Arg Ser Trp  
100 105 110

Leu Asn Ser Asp Ser Leu Lys Ser Ile Arg Tyr Lys Ile Val Asn Phe  
115 120 125

Asp Pro Lys Leu Leu Glu Gly Lys Val Lys Glu Asp Pro Asp Gln Gly  
130 135 140

Glu Ser Met Lys Pro Val Ile Phe Leu Pro Phe Thr Ile Gln His  
145 150 155

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

GCCGACCGAA GAGGCTGGAC ATGACACCAG TGGCATATCA CGGCCATGGG GTCTCAGCAT 60  
TCCGCTGCTG CTCGCCCTC CTCCTGCAGG CGAAAGCAAG AAGATGACAG GGACGCTTTG 120  
CTGGCTGAAC GAGAGCAGGA AGAAGCCATT GCTCAGTTCC CATATGTGGA ATTCACCGGG 180  
AGAGATAGCA TCACCTGTCT CACGTGCCAG GGGACAGGCT ACATTCCAAC AGAGCAAGTA 240  
AATGAGTTGG TGGCTTTGAT CCCACACAGT GATCAGAGAT TGGCCCTCTA CGGAAGTAAG 300  
CAATATGTCC TCCGTGCCAT CCTGCTTTGT CTCCTGGCAT CTGTTTGGT GGTTCCTTC 360  
CTGTTTCCGC ATTCAGTCCT TGTGGATGAT GACGGCATCA AAGTGGTGAA AGTCACATT 420  
AATAAGCAAG ACTCCCTTGT AATTCTCACC ATCATGGCCA CCCTGAAAT CAGGAACCTC 480  
AACTTCTACA CGGTGGCAGT GACCAGCCTG TCCAGCCAGA TTCAGTACAT GAACACAGTG 540  
GTGAATTTTA CCGGGAAGGC CGAGATGGGA GGACCGTTT CCTATGTGTA CTTCTTCTGC 600  
ACGCTACCTG AGATCCTGGT GCACAACATA GTGATCTTCA TGGCAACTTC AGTGAAGATT 660  
TCATACATTG GCCTCATGAC CCAGAGCTCC TTGGAGACAC ATCATATGT GATTGTGGA 720  
GGAAATTTCA CAGCTATTTA ACAACTGCTA TTGGTTCTTC CACACAGCGC CTGTAGAAGA 780  
GAGCACAGCA TATGTTCCCA AGGCCTGAGT TCTGGACCTA CCCCCACGTG GTGTAAGCAG 840  
AGGAGGAATT GGTTCACCTA ACTCCAGCA AACATCTCTC TGCCACTTAG GAGGAAACAC 900  
CTCCCTATGG TACCATTTAT GTTCTCAGA ACCAGCAGAA TCAGTGCCTA GCCTGTGCC 960  
AGCAAAATAGT TGGCACTCAA TAAAGATTG CAGAATTAA TACAGATCTT TTCAGCTGTT 1020  
CTTAGGGCAT TATAAATGGA AATCATACAG TGGTTCTAGG TTATCAAACC ATGGAGTGAT 1080  
GTGGAGCTAG GATTGTGAGT GACCTGCAGG CCATTATCAG TGCTCATCTC GTGCAGAAGT 1140  
GGCAGCAGAG AGGGACCATC CAAATACCTA AGAGAAAACA GACATAGTCA GGATATGAAT 1200  
TTGTTTCAGC TGTTCCTCAA GGCCCTGGAG CTTTTTGAAA AGAAAGAAAA AAGTGTGTTG 1260  
GCTTTTCTTT TTTTGTAGAA GTTAGAATTG TTTTACCAG GAGTCTATGT GGGCCTTGAT 1320  
TCACCTTCA TCCATTGGCT GGAACATGGA TTGGGGATTT GATAGAAAAA TAAACCTGTC 1380  
TTTTGATTCA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAA 1425

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Met Gly Ser Gln His Ser Ala Ala Ala Arg Pro Ser Ser Cys Arg Arg  
1 5 10 15  
Lys Gln Glu Asp Asp Arg Asp Gly Leu Leu Ala Glu Arg Glu Gln Glu  
20 25 30  
Glu Ala Ile Ala Gln Phe Pro Tyr Val Glu Phe Thr Gly Arg Asp Ser  
35 40 45  
Ile Thr Cys Leu Thr Cys Gln Gly Thr Gly Tyr Ile Pro Thr Glu Gln  
50 55 60  
Val Asn Glu Leu Val Ala Leu Ile Pro His Ser Asp Gln Arg Leu Arg  
65 70 75 80  
Pro Gln Arg Thr Lys Gln Tyr Val Leu Leu Ser Ile Leu Leu Cys Leu  
85 90 95  
Leu Ala Ser Gly Leu Val Val Phe Phe Leu Phe Pro His Ser Val Leu  
100 105 110  
Val Asp Asp Asp Gly Ile Lys Val Val Lys Val Thr Phe Asn Lys Gln  
115 120 125  
Asp Ser Leu Val Ile Leu Thr Ile Met Ala Thr Leu Lys Ile Arg Asn  
130 135 140  
Ser Asn Phe Tyr Thr Val Ala Val Thr Ser Leu Ser Ser Gln Ile Gln  
145 150 155 160  
Tyr Met Asn Thr Val Val Asn Phe Thr Gly Lys Ala Glu Met Gly Gly  
165 170 175  
Pro Phe Ser Tyr Val Tyr Phe Phe Cys Thr Val Pro Glu Ile Leu Val  
180 185 190  
His Asn Ile Val Ile Phe Met Arg Thr Ser Val Lys Ile Ser Tyr Ile  
195 200 205  
Gly Leu Met Thr Gln Ser Ser Leu Glu Thr His His Tyr Val Asp Cys  
210 215 220  
Gly Gly Asn Ser Thr Ala Ile



## (2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1921 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

CTTCCAAAGA GCGACTCTTA CTGTTTCTCA TGGTGAGAAG ACAATATTG CTTTCTCTTT	60
TTCTTTCTT CCGGATGAGA GGCTAAGCCA TAATAGAAAG AATGGAGAAT TATTGATTGA	120
CCGTCTTTAT TCTGTGGGCT CTGATTCTCC AATGGGAATA CCAAGGGATG GTTTTCCATA	180
CTGGAACCCA AAGGTAAAGA CACTCAAAGA CAGACATTTT TGGCAGAGCA TAGATGAAAA	240
TGGCAAGTTC CCTGGCTTTC CTTCTGCTCA ACTTTCATGT CTCCTCCTCT TGGTCCAGC	300
TGCTCACTCC TTGCTCAGCT CAGTTTCTG TGCTTGGACC CTCTGGGCCC ATCCTGGCCA	360
TGGTGGGTGA AGACGCTGAT CTGCCCTGTC ACCTGTTCCC GACCATGAGT GCAGAGACCA	420
TGGAGCTGAA GTGGGTAAAG TCCAGCCTAA GGCAGGTGGT GAATGTGTAT GCAGATGGAA	480
AGGAAGTGA AGACAGGCAG AGTGCACCGT ATCAGGGGAG AACTTCGATT CTGCGGGATG	540
GCATCACTGC AGGGAAGGCT GCTCTCCGAA TACACAACGT CACAGCCTCT GACAGTGGAA	600
AGTACTTGTG TTATTTCCAA GATGGTGACT TCTATGAAA AGCCCTGGTG GAGCTGAAGG	660
TTGCAGCACT GGGTTCTAAT CTTACGTCG AAGTGAAGGG TTATGAGGAT GGAGGGATCC	720
ACCTGGAGTG CAGGTCCACC GGCTGGTACC CCCAACCCCA AATACAGTGG AGCAACGCCA	780
AGGGAGAGAA CATCCAGCT GTGGAAGCAC CTGTGGTTGC AGACGGAGTG GGCCTATATG	840
AAGTAGCAGC ATCTGTGATC ATGAAAGGCG GCTCCGGGGA GGGTGTATCC TGCATCATCA	900
GAAATTCCTT CCTCGGCTGT GAAAAGACAG CCAGCATTTT CATCGCAGAC CCCTTCTTCA	960
GGAGCGCCCA GCCCTGGATC GCAGCCCTGG CAGGGACCCT GCCTATCTTG CTGCTGCTTC	1020
TCGCCGGAGC CAGTTACTTC TTGTGGAGAC TACAGAAGGA AATAACTGCT CTGTCCAGTG	1080
AGATAGAAAG TGAGCAAGAG ATGAAAGAAA TGGGATATGC TGCAACAGAG CGGGAAATAA	1140
GCCTAAGAGA GAGCCTCCAG GAGGAACTCA AGAGGAAAAA AATCCAGTAC TTGACTCGTG	1200

GAGAGGAGTC TTCGTCCGAT ACCAATAAGT CAGCCTGATG CTCTAATGGA AAAATGGCCC 1260  
TCTTCAAGCC TGCCTGATTT TTCTGTCATG GGAAGAGSCG ACATGNGCC CTGAGGTCC 1320  
CTTCCCAGGA CNGCTCCAGG ATCGAGATCA CTGTGAGTGG TTGTGGAGTT AAGACCCCTA 1380  
TGGACTCCTT CCCAGCTGAT TATCAGAGCC TTAGACCCAG CACTCCTGG ATGGCTCTG 1440  
CAGAGTGTCT TGGTTGAGAG AATAACGTTG CAGTTCAC AGGSCATGTG ACTTTGAAAG 1500  
AGACTAAAGG CCACACTCTG TTAATAATGG GGCACATATG TGTTCCACC CCACAAATGT 1560  
GATAAGTGTAT CGTGCAGCCA GAGCCAGCCT TCCTTCAGTC AAGGTTTCCA GGCAGAGCAA 1620  
ATACCCTAGA GATTCTCTGT AATATTGGTA ATTTGGATGA AGGAAGCTAG AAGAATTACA 1680  
GGGATGTTTT TAATCCCACT ATGGACTCAG TCTCCTGGAA AAGGATCTGT CCACCTCTGG 1740  
TCATTGGTGG ATGTTAAACC CATATTCCTT TCAACTGCTG CCTGCTAGGG AAAACTGCTC 1800  
CTCATTATCA TCACTATTAT TGCTCACCAC TGTATCCCCT CTACTGGGCA AGTGCTTGTC 1860  
AAGTCTAGT TGTCAATAA ATTTGTTAAT AATGCTGAAA AAAAAAAAAA AAAAAAAAAA 1920  
A 1921

(2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 334 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Met Lys Met Ala Ser Ser Leu Ala Phe Leu Leu Leu Asn Phe His Val  
1 5 10 15  
Ser Leu Leu Leu Val Gln Leu Leu Thr Pro Cys Ser Ala Gln Phe Ser  
20 25 30  
Val Leu Gly Pro Ser Gly Pro Ile Leu Ala Met Val Gly Glu Asp Ala  
35 40 45  
Asp Leu Pro Cys His Leu Phe Pro Thr Met Ser Ala Glu Thr Met Glu  
50 55 60  
Leu Lys Trp Val Ser Ser Leu Arg Gln Val Val Asn Val Tyr Ala  
65 70 75 80  
Asp Gly Lys Glu Val Glu Asp Arg Gln Ser Ala Pro Tyr Arg Gly Arg

85										90				95			
Thr	Ser	Ile	Leu	Arg	Asp	Gly	Ile	Thr	Ala	Gly	Lys	Ala	Ala	Leu	Arg		
100								105				110					
Ile	His	Asn	Val	Thr	Ala	Ser	Asp	Ser	Gly	Lys	Tyr	Leu	Cys	Tyr	Phe		
115								120				125					
Gln	Asp	Gly	Asp	Phe	Tyr	Glu	Lys	Ala	Leu	Val	Glu	Leu	Lys	Val	Ala		
130				135								140					
Ala	Leu	Gly	Ser	Asn	Leu	His	Val	Glu	Val	Lys	Gly	Tyr	Glu	Asp	Gly		
145				150				155				160					
Gly	Ile	His	Leu	Glu	Cys	Arg	Ser	Thr	Gly	Trp	Tyr	Pro	Gln	Pro	Gln		
				165				170				175					
Ile	Gln	Trp	Ser	Asn	Ala	Lys	Gly	Glu	Asn	Ile	Pro	Ala	Val	Glu	Ala		
180								185				190					
Pro	Val	Val	Ala	Asp	Gly	Val	Gly	Leu	Tyr	Glu	Val	Ala	Ala	Ser	Val		
195				200								205					
Ile	Met	Lys	Gly	Gly	Ser	Gly	Glu	Gly	Val	Ser	Cys	Ile	Ile	Arg	Asn		
210				215								220					
Ser	Leu	Leu	Gly	Leu	Glu	Lys	Thr	Ala	Ser	Ile	Ser	Ile	Ala	Asp	Pro		
225				230				235				240					
Phe	Phe	Arg	Ser	Ala	Gln	Pro	Trp	Ile	Ala	Ala	Leu	Ala	Gly	Thr	Leu		
				245				250				255					
Pro	Ile	Leu	Leu	Leu	Leu	Leu	Ala	Gly	Ala	Ser	Tyr	Phe	Leu	Trp	Arg		
260								265				270					
Leu	Gln	Lys	Glu	Ile	Thr	Ala	Leu	Ser	Ser	Glu	Ile	Glu	Ser	Glu	Gln		
275				280								285					
Glu	Met	Lys	Glu	Met	Gly	Tyr	Ala	Ala	Thr	Glu	Arg	Glu	Ile	Ser	Leu		
290				295								300					
Arg	Glu	Ser	Leu	Gln	Glu	Glu	Leu	Lys	Arg	Lys	Lys	Ile	Gln	Tyr	Leu		
305				310				315				320					
Thr	Arg	Gly	Glu	Glu	Ser	Ser	Ser	Asp	Thr	Asn	Lys	Ser	Ala				
				325				330									

(2) INFORMATION FOR SEQ ID NO:135:

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

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AATGGTTCCA GCCTTAATGG AGAAGCCAGT TTCCTTTTTC TTGTTGTTTT ATIGTTTTTA 60
AGCCTCTCTC TGGTTTTTCAG TAGAGTTTGA CCTTAAATAT CATCTTTGTA TACTATTGGT 120
GTCCTTGTAG TTAAGGTCCTT TGCAAAAGTT TGAGTGCAGT TTTTAAGCTA AAAACACGTT 180
TTTTAACTTT CACAAATTTT GTAAGATGAC AATAGCATTG TGTAACATAG ACATTATTGGT 240
AATAGTAGATT TTCTCTCCAT CCCTATTTTG TCCAGCGATT TCCAAGTTAT AAGACGTGAA 300
TAAGACTAAC CGCTCACTTC CACCAGCAGC TGACCTGGTG GGCTTTTGAG TTCAAAGAGT 360
CATTTCCTCA TCTTACCTCC AGCACTGCGA GGCCGTGTGA CCTTGAGAGC CCTTGTTCCT 420
CATTGATGAA AGGAGCTCAT GCCTCATGAA GCCACTGGTA AGGCCATGAG AGCTCACGGG 480
CCATCAAGCT TCCTTCCCAT CACTTGTGGG TGGGAATTGAC ATTACCCGAT GAGCTCTTCC 540
TGGGGTCACC TGGGAGGGAG TGGCCCATGG GTGGTATGAC AAAATCTCAT AGTCAGTCTT 600
TGCAGTTCCT TCCACAGGTA AAATGAGATT TTGAAAAATT TTCATTGTGT TGTATTGTGC 660
CCAAGGTGAG TCTTACATAT TTGAGCAAC AAAACGAAGA TCATTATGAA AATGTCCTTA 720
TGGAAACACT CTAGGGCCAT TGCTCATTTC TATGAGTCTT CGTGCTAAGT CCCTGAGTAC 780
TGTGGCTCAT GTCTTAGCTG GCTAAATCAC AGTCAAAATT CTCTTCTTAA GCCTCAAAAT 840
AAGCTGTGTA TTATACTGCC TGTGGCCAG ACTAATCAAA TACATTGATG GTTTTAGCTG 900
ACTCAGATA CTTTTCTCTC CTCTCTCTTG GTTCTTTAAC TGTCATCCCA GATCTGCGAC 960
ATGCAATAAG GAAAACTGAG TCAGGGAGGA AGTAGGATTC CTTTGTCTGC TAGGAACCA 1020
GTTAGCTTTG GATTGTCCAT AGAATGCACC CTTAACAGTT CTGGAAGAAAT GGATGATATT 1080
TGGTTCCCTGC CCCATGTTCA GTGTCTCTTG GCAGCTGCAA AGCATATCTC AGCTAGAATC 1140
CTTATCGTCT TGAAGTTTCA CAAAGATTTT GAACAGTCAT GGTGGAGATA CAACCTAAGT 1200
ACATTCAATG CATTAGAGC AATCCTTTTG TTTGAGCGAG GGAAGGAGGA ATAAACACAT 1260
GAATATATTT TATTGAATCC CAGAGACCCCT GAAACACCAA GACTCATTTA TATATGCATA 1320
CATGTAGGCG AGAATAATAA ACCTCACCCT ACCTGTCACT GTACTCTCAG TTTTTAAGGT 1380
TCTCCAAAAA CAGGGAAACT GAAAAAATACT TGGGCAGAAA GAAAATATCA TCAAAATACA 1440
CCTATTTCCT TTCAGCTATA GAGATGGCTG GATATCAAAA GCACCCGCGG AGCTTTGCAA 1500
TTTGCTGCTC TTTTCAGCCC TCAGCTTGAC TCTCAGTTTT CAAGAGGGAG AAAATGAATG 1560
TTTCCAGCA TTCTCTGTCC TTTGCTCCAA AGAAGAGAGC AGGTGTTGGC TTCCAAACCT 1620
TCCGATTTTT CTTATTGCTG TTAGGGGGAT CAACTGCATG TTTCTGTAGG GAAAAGGGTG 1680
GCTCACTGAC CTACTTGAAG GCATCTCTC AGTGGAAGCT GGGCAAGAGA ATCCAGGGAT 1740
TTCTTTTGCA GGTTCCTGCG CAGTGCCCTT GCCATCAAGC TGCCTAAAAA TGCAATATTG 1800
CTTCCCTGCG TTTCAAGAGT GGTAATATTG GGGCAAGTGG TGGAGGATCT AAAAAA 1865
AAAAA

```

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

```

Met Asn Val Ser Gln His Ser Leu Ser Phe Ala Pro Lys Lys Arg Ala
1          5          10          15

Gly Val Gly Phe Gln Thr Phe Arg Ile Phe Leu Leu Leu Gly Gly
          20          25          30

```

Ser Thr Ala Cys Phe Leu Arg Glu Lys Gly Gly Ser Leu Thr Tyr Leu  
 35 40 45  
 Lys Ala Phe Ser Gln Trp Lys Leu Gly Lys Arg Ile Gln Gly Phe Leu  
 50 55 60  
 Leu Gln Val Ser Ala Gln Cys Pro Cys His Gln Ala Ala  
 65 70 75

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2094 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

TATGATTATTG ACAGCATGGT ATAATGAAAA GAGCAGTTGG ACCAGAAGGT AAATTCCTAGT 60  
 CCAGATTTTG ACATTTAGAT GTGTATATAT GGGAAAGTTT CTTAAAACCT CGAGTTAAAT 120  
 TTTCCTCATCT GTGAAATAAA GGGATTGGAC TAGATACTCT TTAATAGATA TTCCTTATAT 180  
 GCTTGCTCTCC TTCTAGGTCT AAAATTCTGA TCCTTTAGTA GTTTATAAAT GATTATTGGT 240  
 ATCATTTTCA TCATTTTAGG AGCTCTTTTT TAAAAAATTA TTATTATTTT TTTTGCTCTG 300  
 TAGCCCATTT CTAGAACATC TTGGGAGTTC TAATTATGTT TTAGATAACA TAAAAAGCAT 360  
 AGAATCAGAC ATAGTTAAGC AAGAATTTCa CTTAGTTCCC TAGTTTTTAC AGTCTAAATA 420  
 CATTTTTCTT TCTTTAAAC TGGAGGTTAC TGATACCACC ATTTTCGTCA CCAACAGCCT 480  
 AATAATTCAC AAAGCTATTT GCTAATTTTT GACACTTTTT TCTTTGCCAG TACCATTAAAG 540  
 GGATTTGAAT TTTTTGAGG TTCCATGTTT ATTTCTTTAG TTATGAGTAT GACCTTGGAC 600  
 AAGTTACTTC TCTGACCCTG TAAAGTGAGA GTAAAAATAAC ATCTAGTTCA TAGGGTTGTT 660  
 GACTAGTACC TGGCCCATGG TAATCACTGT GTCATGTTGG CTGTTACTAC CCTTTAAACAT 720  
 GAITTTGCTCC CTTCCCTGTG GTAAAAAGTA TTCATTGGCA CTACTAATA ATCTGTTAGC 780  
 TCAACATATA CTAACCCAAA TGGAAATTTG TTTTGTGAAA TACAATTGTC AGTTCCTTTT 840  
 CATTATAAGA AACGTTAGTT TATTAGTAGT ATATACCCCT GAGAAAGCAC TAATTTAATT 900  
 TGAATTTGAG TGGATTAATT CATAATATGA AAGCTGAGAA TGTAGATTGT CTCTCTCTCT 960  
 TATTTTGAAT AGTTCATAGA ATAATTTATT TCTTTTATCT GGGAAACAAA ATAACCTGGT 1020  
 TAATTTGTGA CATTCTCAAA CATATTTTAC AAGTTTAGAT AAGTTGAGAA TGGCAAAAAC 1080  
 CACAATTACT TTTGCAACAA TCTAATACTT TTAGAAGAAA AATCTATCTT ACCTTATTTT 1140  
 ATACTAAAAA AAAAAAAGAG GCGCAAGAG GCCTACAGGA TTTTGAGATG TAAGAACACA 1200  
 TATTTAATTC CCTCTATGCT CTTGGTTCTT CCCTCTCTTT CCACGTTGGA TAACAATTTT 1260  
 TTGGTTGTTT TGTTTAAAGT GGTGCTCTGA AGCTTAATCT CAGTACCCCT TACTCTGAAT 1320  
 TGTCAAATTT TGATAAACG TGCCATTTTC TTTGGTAAGA GAAAGCAGGT CTTAATGTCT 1380  
 GCCAGAACAC AATTATATAT CTTATTGGC TTCAATTAAC TTTTAGAAAA CTTTAGCATT 1440  
 TGTACTTTTT TTCCATTGCA TTTACTTTCA AATGCACCTA ATGAATTCGT CACCCAGCTG 1500  
 CAACTTTTCC CTCTCTGTC CCATTGCTTT CTCCTTTCCC CGACGCACAG AATAACATG 1560  
 AAGCTCAGCA GTAGAAGCGT AATGATTTCC CTCAGGAAAA ACTTCTGACA GCTAGGTTTT 1620  
 TCAAGGGTTT CCTGTGCTA GCTGAGATGC AAAACAAATC ATGGAAGATT GCATACCTGT 1680  
 GTGGTATTTT AAAACAAGT TGACTTTTTC AGTTTCTTGA ACGGTTAAGG GTGGATTAA 1740  
 AAACATGACA GTTTAGTTT GGGGAACAGA AGCTCTCTTC GTCTTAAAGC AGATTCTCTG 1800  
 ATTCTTTTAG ACGTCATAGC TCCTTAGTTC TGCTCCGTGC GCCCTAACTT GGCATGGGCA 1860  
 AGTTGAAGTT CATCTTAGA CTCGAGCGTT CTGAGCATGG CTGAAGTATT AAAATGTTTA 1920

ATATTTTTTA GAGCAAAATT GATGGAAAGC ATTTGGCTGA ATCTAAAGAC CTGCAGTCAG 1980  
 ATTCTTCAAT GTGGTTTACC CAACTGGAGT AGTGATAAAC ACCTTAAATCA TAAAAATGAAT 2040  
 AAAAAACAAA AAACCAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAA 2094

(2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 77 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Met Ser Ala Arg Thr Gln Phe Ile Cys Leu Ile Gly Phe Ile Lys Leu  
 1 5 10 15  
 Leu Glu Asn Phe Ser Ile Cys Tyr Phe Phe Pro Leu His Leu Leu Ser  
 20 25 30  
 Asn Ala Pro Asn Glu Phe Val Thr Gln Ser Gln Leu Phe Pro Ser Leu  
 35 40 45  
 Ser His Cys Phe Leu Leu Ser Pro Thr His Arg Ile Asn Met Lys Leu  
 50 55 60  
 Ser Ser Arg Ser Val Met Ile Ser Leu Arg Lys Asn Phe  
 65 70 75

(2) INFORMATION FOR SEQ ID NO:139:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2069 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

AAATTCAACA TAAACCCAAA TCTGTACTTC TCCAGAGGAG CAGCTCTGAG GTAGAAATTA 60  
 CAACGATGAA AAGAGCACAA CGTACAAAAC CAAGAAAGAG TCTGTTGTGT GAAGGGTCAT 120  
 TCGATGAAGA AGCTTCTGCA CAGTCCTTTC AGGAAGTGTT AAGTCAATGG AGAACCGGAA 180  
 ATCATGATGA CAACAAGAAA CAGAATTTC ATGCAGCAGT AAAAGACTCA TTGGAAGAAT 240  
 GCCAAGTACA GACTAATCTG AAAATTGGA GAGAACCACCT TAATATTGAA CTTAAAGAAG 300  
 ACATTCTATC CTATATGGAA AAATTATGGC TTAAAAACA CAGGAGAACT CCACAAGAGC 360  
 AACTTTTTAA AATGCTACCA GATACGTTCC CACATCCACA TGAAACCACT GGTGATGCAC 420

AGTGTCTCTCA AAATGAAAC GATGAAGATA GTGATGGTGA GGAGACCAAA GTACACAACA 480  
 CAGCTCTTTT ATTGCAGTA GAACATTAA ACATAGAGAG ACCTGAACCA TCTCTAAAGA 540  
 TAGTCGAAGT GGTATGATCT TATGAAGAGG AATTGTGAAGA AGCAGAAAAAT ATTGTGCTCT 600  
 ACAAGGTAA ATTAGCTGAT GCAGACAGTC AACGAAGTTG TGCTTTTCAT GATTGTGAGA 660  
 AGAATAGCTT TCCATATGAA AATGGCATCC ATCAACATCA TGTTTTTCAT AAGGGAAAGA 720  
 GAGACTTCTT AAATCTTTGT CTGAGAAACA GCTATACTTA TTATAAAGAT AATTCAAAG 780  
 CAGAACTTC AAACAGAGT TTTGACAACA TCGTGGATCC TGATGTGTAT TCTTCTGACA 840  
 TTGAAAAAAT TGAGGAAAGC ACCTCCTTTG AAAGAAATTT AAAGGAGAAA AATATAGGTT 900  
 TAGAAAGTAA TCAAAAGTCT GATGATTCTT GTGTATCACT TGAAGCAAG GACACTTTGC 960  
 TAGGTAGAGA TTTAGAAAAA GCTCCCATG AGGAGAAATTT ATCTCAAGAC ATCAAAGAT 1020  
 CCTTGGAAAT GAGCAATCTG TATAAGAGGC CAAGCTTTGA AGAATCAAAA ACTCAAAAGT 1080  
 CATCACTGTT GTTACAAGAA ATAGCCTGCA GAAGTAAGCC TATAACAAAA CAATATCAAG 1140  
 GACTTGAAGG ATTCTTTAT TTTGATACAA ATGAAAGACT CAACTTACTT CCTTCTCATC 1200  
 GTTTAGAATG CAACAATTCC AGTACTAGGA TTACACTTGC AGAAGACAGA GAATGGATT 1260  
 CAGACCATAG CTTAAGTGAA TATGCTGATA ATGCAATTGT CTTGGGTGTT CTGAGGGTG 1320  
 CTCAGAGTCC ATCATCAAGT AGAAAAACAG AAAAGATGGG TCAGAAATCA CAGAGACCTT 1380  
 CAACAGCAAA TTTTCCACTT TCCAACTCTG TTAAGAAAAA CTCGAGTTGC CTTTCTCTC 1440  
 CTCATCTCTG ATCAAGAAAT GCAGCTGCTC AATCATCATC TAGAGCTGCT TCTGAAATTT 1500  
 CAGAAAAATG ATATATTGAT ATTACTGACC AGAATGAGCT TTCTTTAGAT GACACTACTG 1560  
 ATCAACATAC TTTAGACAAT TTGAAAAAAG AATTACAAGT GCTGAGATCT CTTGCAGATA 1620  
 CTTTCAGAAA GCTTTACAGC TTAACCTCAG AAGAGTTCCC AGATTTCAGC AGCCAAATC 1680  
 TGAATATAAG TCAGATTTCC ACAGATTTCC TTAAGACCTC ACATGTGAGG GGTCCCTGTG 1740  
 GAGTTGAGGA ATTGAGCTGT TCTGGAAGAG ATACCAAAAT TCAGTCTTTG CTGTCACTTT 1800  
 CTGAGAGCAG TACAGAGTAG GAGGAGGAAG ATTTTCTCAA CAAGCAACAT GTGATCACAC 1860  
 TACCGTGGTC AAAGAGTACT TAAAGATTAT TTGTTGATT CTGTTTCCAT TTTGTACCCA 1920  
 GAGTAAAGCA ACAAAGTAGG AAAAGTAAGC AAGTGATTAC CTATCCAAGT CTTGGAGATT 1980  
 TTGATTACTA ATGCTCTTGA TGTTCAGG CTACAAACTA ATAAAGTAA AATTATAAGT 2040  
 TCAAAAAAAA AAAAAAAA AAAAAAAA 2069

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 605 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Met Lys Arg Ala Gln Arg Thr Lys Pro Arg Lys Ser Leu Leu Cys Glu  
 1 5 10 15  
 Gly Ser Phe Asp Glu Glu Ala Ser Ala Gln Ser Phe Gln Glu Val Leu  
 20 25 30  
 Ser Gln Trp Arg Thr Gly Asn His Asp Asp Asn Lys Lys Gln Asn Leu  
 35 40 45  
 His Ala Ala Val Lys Asp Ser Leu Glu Glu Cys Glu Val Gln Thr Asn  
 50 55 60  
 Leu Lys Ile Trp Arg Glu Pro Leu Asn Ile Glu Leu Lys Glu Asp Ile  
 65 70 75 80

Leu Ser Tyr Met Glu Lys Leu Trp Leu Lys Lys His Arg Arg Thr Pro  
 85 90 95  
 Gln Glu Gln Leu Phe Lys Met Leu Pro Asp Thr Phe Pro His Pro His  
 100 105 110  
 Glu Thr Thr Gly Asp Ala Gln Cys Ser Gln Asn Glu Asn Asp Glu Asp  
 115 120 125  
 Ser Asp Gly Glu Glu Thr Lys Val Gln His Thr Ala Leu Leu Leu Pro  
 130 135 140  
 Val Glu Thr Leu Asn Ile Glu Arg Pro Glu Pro Ser Leu Lys Ile Val  
 145 150 155 160  
 Glu Leu Asp Asp Thr Tyr Glu Glu Glu Phe Glu Glu Ala Glu Asn Ile  
 165 170 175  
 Val Pro Tyr Lys Val Lys Leu Ala Asp Ala Asp Ser Gln Arg Ser Cys  
 180 185 190  
 Ala Phe His Asp Cys Gln Lys Asn Ser Phe Pro Tyr Glu Asn Gly Ile  
 195 200 205  
 His Gln His His Val Phe Asp Lys Gly Lys Arg Asp Phe Leu Asn Leu  
 210 215 220  
 Cys Leu Arg Asn Ser Tyr Thr Tyr Tyr Lys Asp Asn Ser Lys Ala Glu  
 225 230 235 240  
 Thr Ser Asn Thr Asp Phe Asp Asn Ile Val Asp Pro Asp Val Tyr Ser  
 245 250 255  
 Ser Asp Ile Glu Lys Ile Glu Glu Ser Thr Ser Phe Glu Arg Asn Leu  
 260 265 270  
 Lys Glu Lys Asn Ile Gly Leu Glu Ser Asn Gln Lys Ser Asp Asp Ser  
 275 280 285  
 Cys Val Ser Leu Glu Ser Lys Asp Thr Leu Leu Gly Arg Asp Leu Glu  
 290 295 300  
 Lys Ala Pro Ile Glu Glu Lys Leu Ser Gln Asp Ile Lys Glu Ser Leu  
 305 310 315 320  
 Glu Leu Ser Asn Leu Tyr Lys Arg Pro Ser Phe Glu Glu Ser Lys Thr  
 325 330 335  
 Thr Lys Ser Ser Leu Leu Leu Gln Glu Ile Ala Cys Arg Ser Lys Pro  
 340 345 350  
 Ile Thr Lys Gln Tyr Gln Gly Leu Glu Arg Phe Phe Ile Phe Asp Thr  
 355 360 365  
 Asn Glu Arg Leu Asn Leu Leu Pro Ser His Arg Leu Glu Cys Asn Asn  
 370 375 380



Ser Ser Thr Arg Ile Thr Leu Ala Glu Asp Arg Glu Trp Ile Pro Asp  
 385 390 395 400  
 His Ser Leu Ser Glu Tyr Ala Asp Asn Ala Ile Val Leu Gly Val Leu  
 405 410 415  
 Gln Gly Ala Gln Ser Pro Ser Ser Ser Arg Lys Gln Gln Lys Met Gly  
 420 425 430  
 Gln Lys Ser Gln Arg Pro Ser Thr Ala Asn Phe Pro Leu Ser Asn Ser  
 435 440 445  
 Val Lys Glu Ser Ser Ser Cys Leu Ser Ser Ser His Pro Arg Ser Arg  
 450 455 460  
 Ser Ala Ala Ala Gln Ser Ser Ser Arg Ala Ala Ser Glu Ile Ser Glu  
 465 470 475 480  
 Ile Glu Tyr Ile Asp Ile Thr Asp Gln Asn Glu Leu Ser Leu Asp Asp  
 485 490 495  
 Thr Thr Asp Gln His Thr Leu Asp Asn Leu Glu Lys Glu Leu Gln Val  
 500 505 510  
 Leu Arg Ser Leu Ala Asp Thr Ser Glu Lys Leu Tyr Ser Leu Thr Ser  
 515 520 525  
 Glu Glu Phe Pro Asp Phe Ser Ser Gln Ser Leu Asn Ile Ser Gln Ile  
 530 535 540  
 Ser Thr Asp Phe Leu Lys Thr Ser His Val Arg Gly Pro Cys Gly Val  
 545 550 555 560  
 Glu Glu Leu Ser Cys Ser Gly Arg Asp Thr Lys Ile Gln Ser Leu Leu  
 565 570 575  
 Ser Leu Ser Glu Ser Ser Thr Asp Glu Glu Glu Glu Asp Phe Leu Asn  
 580 585 590  
 Lys Gln His Val Ile Thr Leu Pro Trp Ser Lys Ser Thr  
 595 600 605

(2) INFORMATION FOR SEQ ID NO:141:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4337 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GTCTCTGGATG GCGGAGCCTT GGGTTCGGG GGCCTGGGAC CTGCAACTCT TTCTACAAGA 60

TATCAAGTTA TTCTAGTACA ACCATATAAA TAAATAATAC CTGAAGTCTC AGTGTAAACAT 120  
 GGACAATTA CAGTGTATGAC AGATAAATAC AGACGCATGG GGATCAAATA CTAGGCAAAA 180  
 CGCTTTTTAA AAGTGTATCA GGCTTTTAAAG AAACACTGCA GGATCCTGTC TATCTTAAATG 240  
 CTGATAGAGC TCAGCTAAAA ATTTAGGAGG TTCTAGTATT CTTCATGGCT GAAGCTGAGA 300  
 GAGTCTGAAA CCCTGATGCT TAAGCTCCAT TCTAGATCAT AGCTCCAACCT CCTTCAGGAT 360  
 ATAAGGAAAA GAGATTATAT TTCCACAATG ATAGATCTTT GGTGTGTACAG GTTTCCCAAT 420  
 GAGTGGATCA TGATGACCGT ATTGTAGGGA CTGGCCATAG TATGGCTGCT TCCCGATCTA 480  
 CTCGTGTGTA MAGATCAACA GTGGGGTTAA ACGGCTTGGA TGAATCTTTT TGTGGTAGAA 540  
 CTTTAAGGAA CTGTAGCATT GCGCATCCCT AGAATACTC TTCTAATCTT CAGTACAGAT 600  
 CAAGATCACC AAAGAAGAGA CCAGAGCCTG TGCCAATTC AAGAGGAAAT AATAATGGGA 660  
 GAACCATCA TTTAAACAG CAGAGTACCC GAGAATCATG GGTAAAGCCT AGGAAAAGAG 720  
 GACTTTCTTC TTCAGAAAAG GATAACATAG AAAGGCAGGC TATAGAAAAT TGTGAGAGAA 780  
 GGCAAAACAGA ACCTGTTTCA CCAGTTTATA AAAGAATTAA GCGTTGTCTT AGATCTGAAG 840  
 CACCAAAACAG CTCAGAAGAA GATTCTCCTA TAAAATCAGA CAAGGAGTCA CAGTACACAGA 900  
 GGAGTACAGT AGTGGAACAT GATGAGATTT TCAAGGGGAC TAAACGAGCT TGTCCGATCTC 960  
 TPTATCTGGA TGATTGTGAG AAAAGGGGAA TTTAAAGGTT GAATGTCACT GAGGAAGGGC 1020  
 CACTTAATTC TGCAGTAGTT GAAGAAATCA CAGGCTATT TTGCTGTCAAT AGTGTGTGATG 1080  
 ACAGTGATTC AGCTGTTTATA AACTGTGATG ACTGTGAGCC TGATGGGAAC CTTAAACAAA 1140  
 ATAGCATTTG TTCTATGTG TTACAGGAAA AATCAGTAGC TGAAAATGGG GATACCGGATA 1200  
 CCCCAACTTC AATGTTCTCT GATAGTAGGA AGGAGGACAG TTATATAGAC CATAGGGTGC 1260  
 CTTGCACAGA TTTCAAGATG CAGGTCAGT TGGAGGACCA CAAAATAGTA ACTGCTCTGT 1320  
 TGCTGTGGA ACATGTTAAT CAGCTGACTA CTGAGCCAGC TACAGGGCCC TTTTCTGAAA 1380  
 CTCAGTCATC TTTAAGGGAT TCTGAGGAGG AAGTAGATGT GGTGGGAGAT AGCAGTGCCCT 1440  
 CAAAAGAGCA GTGTAAAGAA AACACCAATA ACGAAGTGA CACAGTCTT GAGAGTAGTC 1500  
 CAGCCTCCGG AGAAGCTGAA CCACTCTCTG TTCTAGACTG TGATATCAGCT CAAATGATGT 1560  
 TTTTATCAGA ACCCTAAGAA CATGTTTATA CTCTGAGAAC CTCAACAGCA AGGGCAGCCC 1620  
 CTACCAAGAG TAGTCCCAT AAAACAGTT CTCTTACAG AGAAAATGGA CAATTTGAGG 1680  
 AGAATAATCT TAGTCTTAAT GAAACAAATG CAACTGTTAG TGATAATGTA AGTCAATCTC 1740  
 CTACAAATCC TGGTGAAATT TCTCAAATG AAAAAGGGAT ATGTTGTGAC TCTCAAATAA 1800  
 ATGGAAGTGA AGGAGTAAGT AAACCACCCCT CAGAGGCAAG ACTCAATATT GGACATTTGC 1860  
 CATCTGCCAA AGAGAGTGCC AGTCAGCACA TTACAGAAGA GGAAGATGAT GATCCTGATG 1920  
 TTTATTAATT TGAATCAGAT CATGTGGCAG TGAAACACAA CAAAGATTAT CAGAGACTAT 1980  
 TACAGACGAT TGCTGTACTC GAGGCTCAGC GTTCTCAAGC AGTCCAAGAA CTTGAAAAGTT 2040  
 TAGGCAGGCA CCAGAGAGAA GCATGAAAA ATCCCATTTG ATTTGTGGAA AAACCTCAGA 2100  
 AGAAGGCTGA TATTGGCTCT CCATATCCAC AGAGAGTGT TCAATTGCTT GAGATCGTAT 2160  
 GGGACCAATA TACCATAGC CTTGGGAATT TTGAAAGAGA ATTTAAAAAT CGTAAAAGAC 2220  
 ATACTAGAAG AGTTAAGCTA GTTTTGTATA AAGTAGGTTT ACCTGTGTA CCAAAGATGC 2280  
 TTTTATGCTC TAAGAAGGAT GGAGAGTCCC TTTCTATATC TTTGTTGCTT TTGAGTAGTG 2340  
 GTCCAGAGAG CTCAAGCAGT CGTCTCAGA TGATAAGAGG ACGCTGTGTG GATGATACCA 2400  
 AACCTGAAC ACCTTAAACAG TTGTGGACTG TTGAAGAACA GAAAAGAGCT GAACAGCTAC 2460  
 TCAATCAATA CCTCTCTGAA GAAGTAGAAT CTCGACGCTG GCAGAGAGTA CGAGATGAAT 2520  
 TGGGCAACAG CAGACCAAAA CAGGTTGCCA GCCGAGTACA GAAGTATTTC ATAAAGCTAA 2580  
 CTAAGAGTGG CATTTCCAGTA CCAGGACGAA CACCAAACTT ATATATATAC TCCAAAAGT 2640  
 TCTCAACAG CAGAGCAGAC CACCCTCTTA ATAAGCATCT CTTTAAGGCT TCCACTTTCA 2700  
 TGACTTCACA TGAACCCGCA GTGTATATGG ATGAAGATGA TGACCCATCT TGCTTTTCTA 2760  
 GCCACATGAA CACTGCTGTT GAAGATGCAAT CAGATGACGA AAGTATTCCT ATCATGTATA 2820  
 GGAATTTACC TGAATATAAA GAATTTATAC AGTTTAAAAA GTTAAAGAGG CAGAAACTTC 2880  
 AGCAAAATGCA AGCTGAAAGT GGATTGTGTC AACATGTGGG CTTTAAAGTG GATACTGTG 2940  
 CGATAGAACC CATCCAGGGT GTTCGGTGGC ATTTGCCAGGA TTGTCCTCCA GAAATGCTCT 3000  
 TGGATTCTGT TGATTTCTGT TCAGACTGTC TACATGA AAC AGATATTAC AAGGAAGATC 3060  
 ACCAATTAGA ACCTATTATG AGGTGAGAGA CATTCTTAGA CAGAGACTAC TGTGTCTCTC 3120  
 AGGGCACAG TTTCAATTTAT CTTGACCCAA ACTACTTCC CATAGCAATG GTATCATTTG TAATTATGTG 3180  
 GAGAACATCA TTTACTAGTC CTCTTCAACA CATAGCAATG GTATCATTTG TAATTATGTG 3240  
 CACAGTTTGG AAGATTTCTC TGCTTTCCCA GAAATGACAC TCACAGCATG AGAGCTTCTC 3300

69746723 = 123660  
 69746723 = 123660

GAGTGTCTCT GTCAAGTACA GCTCTGCACC GTTGTGGCTC TAGATCACTG TTCAGCAGCT 3360  
 GAACATTCCT GGTGAGCAAA GGTTTCCCTG GTGAATTTT CACCCTGCG TTTTAGTGG 3420  
 TGAICTTAAA TGGGTGAGAT GGAACGAGAG CACACATTAA AGAGAGAGTA AATTCCAAAG 3480  
 GTTTCAAAGA ACTTGGTCAT AAATATGATA ATGAGAAGAC AAAGTATTTA TATTAACA 3540  
 GTTTAGTAGC CTTCAAGTTT GTGAAAATAG TTTTCAGCAC AGAACTGAC TTTCTTAGAC 3600  
 AAAGTTTAA CCAATGATGG TGTGTGCTTC TAGGATATAC ACTTTAAAG AACTCACTGT 3660  
 CCCAGTGGT GTCAATTGATG GCCTTTAGTA AATTGGAGCT GCTTAATCAT ATTGATATCT 3720  
 AATTTCITTT AACCACAATG AATTGTCTT AATTACCAAC AGTGAAGCAC TACAGGAGGC 3780  
 AACTGTGGCA TTGCTTCTT AACCAAGTCA TGGTGTGTGA ATGTTATAAA ATTGTCACTC 3840  
 AGATATATTT TTTAAATGTA ATGTTATATA AGATGATCAT GTGATGTGTA CAAACTATGG 3900  
 TGAAAAGTGC CAGTGTAGT AACTGTGTAA AGTTTCTAAT TCACAACATT AATTCCITTA 3960  
 AAATACACAG CTTCTGCGCT CTGTATTGG AGTTGTCACT ACAACTCATC AAAGAAAACT 4020  
 GCCTAATATA AAAATCATAT ATATGTAAT AATTTCCTC TTTGTAGTC TGCACAAGAT 4080  
 CCATAAAGA TTGTATTTT ATTACTATTT AAACAAGTGA TTAATTTAG TCTGCACAGT 4140  
  
 GAGCAAGGGT TCACATGCAT TCTTTTATAC TGCTGGATTT TGTGTGTCAT CATTAAAAAC 4200  
 ATTTTGTATG TTTCTTCTTA TCTGTGTATA CAGTATGTTT TTGAATGATG TTCATTTGTC 4260  
 AGGAGAAGTGC TGAGAAATAA ACTATGTGGA TACTGTCTGT TMTRTCAAA AAAAAA 4320  
 AAAAAA 4337

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 903 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Met Ala Ala Ser Arg Ser Thr Arg Val Thr Arg Ser Thr Val Gly Leu  
 1 5 10 15  
 Asn Gly Leu Asp Glu Ser Phe Cys Gly Arg Thr Leu Arg Asn Arg Ser  
 20 25 30  
 Ile Ala His Pro Glu Glu Ile Ser Ser Asn Ser Gln Val Arg Ser Arg  
 35 40 45  
 Ser Pro Lys Lys Arg Pro Glu Pro Val Pro Ile Gln Lys Gly Asn Asn  
 50 55 60  
 Asn Gly Arg Thr Thr Asp Leu Lys Gln Gln Ser Thr Arg Glu Ser Trp  
 65 70 75 80  
 Val Ser Pro Arg Lys Arg Gly Leu Ser Ser Ser Glu Lys Asp Asn Ile  
 85 90 95  
 Glu Arg Gln Ala Ile Glu Asn Cys Glu Arg Arg Gln Thr Glu Pro Val  
 100 105 110  
 Ser Pro Val Leu Lys Arg Ile Lys Arg Cys Leu Arg Ser Glu Ala Pro  
 115 120 125

Asn Ser Ser Glu Glu Asp Ser Pro Ile Lys Ser Asp Lys Glu Ser Val  
 130 135 140  
 Glu Gln Arg Ser Thr Val Val Asp Asn Asp Ala Asp Phe Gln Gly Thr  
 145 150 155 160  
 Lys Arg Ala Cys Arg Cys Leu Ile Leu Asp Asp Cys Glu Lys Arg Glu  
 165 170 175  
 Ile Lys Lys Val Asn Val Ser Glu Glu Gly Pro Leu Asn Ser Ala Val  
 180 185 190  
 Val Glu Glu Ile Thr Gly Tyr Leu Ala Val Asn Gly Val Asp Asp Ser  
 195 200 205  
 Asp Ser Ala Val Ile Asn Cys Asp Asp Cys Gln Pro Asp Gly Asn Thr  
 210 215 220  
 Lys Gln Asn Ser Ile Gly Ser Tyr Val Leu Gln Glu Lys Ser Val Ala  
 225 230 235 240  
 Glu Asn Gly Asp Thr Asp Thr Gln Thr Ser Met Phe Leu Asp Ser Arg  
 245 250 255  
 Lys Glu Asp Ser Tyr Ile Asp His Lys Val Pro Cys Thr Asp Ser Gln  
 260 265 270  
 Val Gln Val Lys Leu Glu Asp His Lys Ile Val Thr Ala Cys Leu Pro  
 275 280 285  
 Val Glu His Val Asn Gln Leu Thr Thr Glu Pro Ala Thr Gly Pro Phe  
 290 295 300  
 Ser Glu Thr Gln Ser Ser Leu Arg Asp Ser Glu Glu Glu Val Asp Val  
 305 310 315 320  
 Val Gly Asp Ser Ser Ala Ser Lys Glu Gln Cys Lys Glu Asn Thr Asn  
 325 330 335  
 Asn Glu Leu Asp Thr Ser Leu Glu Ser Met Pro Ala Ser Gly Glu Pro  
 340 345 350  
 Glu Pro Ser Pro Val Leu Asp Cys Val Ser Ala Gln Met Met Ser Leu  
 355 360 365  
 Ser Glu Pro Gln Glu His Arg Tyr Thr Leu Arg Thr Ser Pro Arg Arg  
 370 375 380  
 Ala Ala Pro Thr Arg Gly Ser Pro Thr Lys Asn Ser Ser Pro Tyr Arg  
 385 390 395 400  
 Glu Asn Gly Gln Phe Glu Glu Asn Asn Leu Ser Pro Asn Glu Thr Asn  
 405 410 415  
 Ala Thr Val Ser Asp Asn Val Ser Gln Ser Pro Thr Asn Pro Gly Glu  
 420 425 430

Ile Ser Gln Asn Glu Lys Gly Ile Cys Cys Asp Ser Gln Asn Asn Gly  
 435 440 445  
 Ser Glu Gly Val Ser Lys Pro Pro Ser Glu Ala Arg Leu Asn Ile Gly  
 450 455 460  
 His Leu Pro Ser Ala Lys Glu Ser Ala Ser Gln His Ile Thr Glu Glu  
 465 470 475 480  
 Glu Asp Asp Asp Pro Asp Val Tyr Tyr Phe Glu Ser Asp His Val Ala  
 485 490 495  
 Leu Lys His Asn Lys Asp Tyr Gln Arg Leu Leu Gln Thr Ile Ala Val  
 500 505 510  
 Leu Glu Ala Gln Arg Ser Gln Ala Val Gln Asp Leu Glu Ser Leu Gly  
 515 520 525  
 Arg His Gln Arg Glu Ala Leu Lys Asn Pro Ile Gly Phe Val Glu Lys  
 530 535 540  
 Leu Gln Lys Lys Ala Asp Ile Gly Leu Pro Tyr Pro Gln Arg Val Val  
 545 550 555 560  
 Gln Leu Pro Glu Ile Val Trp Asp Gln Tyr Thr His Ser Leu Gly Asn  
 565 570 575  
 Phe Glu Arg Glu Phe Lys Asn Arg Lys Arg His Thr Arg Arg Val Lys  
 580 585 590  
 Leu Val Phe Asp Lys Val Gly Leu Pro Ala Arg Pro Lys Ser Pro Leu  
 595 600 605  
 Asp Pro Lys Lys Asp Gly Glu Ser Leu Ser Tyr Ser Met Leu Pro Leu  
 610 615 620  
 Ser Asp Gly Pro Glu Gly Ser Ser Ser Arg Pro Gln Met Ile Arg Gly  
 625 630 635 640  
 Arg Leu Cys Asp Asp Thr Lys Pro Glu Thr Phe Asn Gln Leu Trp Thr  
 645 650 655  
 Val Glu Glu Gln Lys Lys Leu Glu Gln Leu Leu Ile Lys Tyr Pro Pro  
 660 665 670  
 Glu Glu Val Glu Ser Arg Arg Trp Gln Lys Ile Ala Asp Glu Leu Gly  
 675 680 685  
 Asn Arg Thr Ala Lys Gln Val Ala Ser Arg Val Gln Lys Tyr Phe Ile  
 690 695 700  
 Lys Leu Thr Lys Ala Gly Ile Pro Val Pro Gly Arg Thr Pro Asn Leu  
 705 710 715 720  
 Tyr Ile Tyr Ser Lys Lys Ser Ser Thr Ser Arg Arg Gln His Pro Leu  
 725 730 735

Asn Lys His Leu Phe Lys Pro Ser Thr Phe Met Thr Ser His Glu Pro  
 740 745 750  
 Pro Val Tyr Met Asp Glu Asp Asp Arg Ser Cys Phe His Ser His  
 755 760 765  
 Met Asn Thr Ala Val Glu Asp Ala Ser Asp Asp Glu Ser Ile Pro Ile  
 770 775 780  
 Met Tyr Arg Asn Leu Pro Glu Tyr Lys Glu Leu Leu Gln Phe Lys Lys  
 785 790 795 800  
 Leu Lys Lys Gln Lys Leu Gln Gln Met Gln Ala Glu Ser Gly Phe Val  
 805 810 815  
 Gln His Val Gly Phe Lys Cys Asp Asn Cys Gly Ile Glu Pro Ile Gln  
 820 825 830  
 Gly Val Arg Trp His Cys Gln Asp Cys Pro Pro Glu Met Ser Leu Asp  
 835 840 845  
 Phe Cys Asp Ser Cys Ser Asp Cys Leu His Glu Thr Asp Ile His Lys  
 850 855 860  
 Glu Asp His Gln Leu Glu Pro Ile Tyr Arg Ser Glu Thr Phe Leu Asp  
 865 870 875 880  
 Arg Asp Tyr Cys Val Ser Gln Gly Thr Ser Tyr Asn Tyr Leu Asp Pro  
 885 890 895  
 Asn Tyr Phe Pro Ala Asn Arg  
 900

(2) INFORMATION FOR SEQ ID NO:143:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1299 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

AATCGGGACC CCATCCCCCA AATCACTGGA TCCTGCAGCC CCACATCCTA AGGTGGATCC 60  
 CAGCCTTCCC TGTGCCCCCT ACTGGATCCT GGACCTCTAC GTCTTAACCA CTGGATCCCA 120  
 CACAAATCAG TGAATGGATC CCAACACCCC AACCACAGGA GCACGGATTC CCTGTACCTC 180  
 AACACCCAGA CCCTGCCTCC CTCAGGCACC AGATCCAAGT TCCTAGTGAA ACGCTGGATC 240  
 CTAGATCCCC AACCCAGAT CCCCATGCCT CGAGCCCTGG ATCTCCAAGC TCAGCTGCTG 300  
 GATTCTGGAT GTCAACAAC CTCACCACTG GATCCTGACA ACCACAATGC CTGGATCCTG 360  
 GGGCCCCCAT CACTGGATCC CAGATCCCT CACTCCACCC ACTGGATTCC TGCATTGGTT 420

TTTGGTTTTT TGTTTTTTTT TTAACCTCGA CACTGGGTCT CAGATCCTTC TGCTGACTGC 480  
 CAGATCCCTG CATTTCAGC ACTACGCCTT CCACCCCCAG GCACTGGATC CCAGATTCCC 540  
 AAGCCTTCAC CCACCAAGATT CTGGCTCCTA AAACAAGTGC GGGGGCCCA GTGGCACAGC 600  
 AAGTGGATCC TGGCAACTGC AGCTGCTGGA TTCCAGATTC TGGGTCCCA ATCCCTCTGC 660  
 CCAGTCCCTC AATGTTGAAA CCTCATCTCT TGAAGGCAGA TCCTGATATT CCAAGGCACT 720  
 GAATCCCAAG CCCTGAATCC CCGGTTTCTG ATCTGAATCT TCCAGGCGCC GGGTCCCAAA 780  
 TGTTCAGGCC CCAAGTCTAG ATCCTGGCAG CCCAGTCACA GAGTATCCCA CACACACTGG 840  
 TGCCCAAGAGC CGGCTTCTCA TGACATGAAA TTGCATGGTC GAGGGAGTCT GTGGGAAGG 900  
 AAGCCCAAGT CCTGGCTGCA ACCTGCACGG ATGCTGGATT CCCCTCACCC CACCTCTGTC 960  
 ATGGCCACCC CCTCCAGCC CTGTGGGAAA ACTGTTCCCT GGAACCACTC CACTCCCTGC 1020  
 ATCCCCACAC TTCACAGCAT CTTCATCCCT CCTCCACTT CTAGGCGAAT AGTCCCAGAG 1080  
 GCTGTGTTCC TCCAAGGGGT CCGAGGAATC ACTCACTCCT GGAGGCTGGC AAGGAGACAG 1140  
 TCTGAGGCCA GGGACACATG AAGGGAATGC CCCACCCAG CACTATCAGG GCCTCCCAAG 1200  
 GCTTCCAGAG TTGAAGGCCA GGAGAAAATC GGCAAGACC ACCCTTCCCT AAACCCAAGC 1260  
 ACCCAATGAT GCRAAAAAAA AAAAAAAAAA AAAAAAAAAA 1299

(2) INFORMATION FOR SEQ ID NO:144:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 98 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

Met Lys Leu His Gly Arg Gly Ser Leu Trp Gly Arg Lys Pro Arg Ser  
 1 5 10 15  
 Trp Leu Gln Pro Ala Arg Met Leu Asp Ser Pro Ser Pro His Leu Cys  
 20 25 30  
 Met Ala Thr Pro Ser Gln Pro Cys Gly Glu Thr Val Pro Trp Asn His  
 35 40 45  
 Ser Thr Pro Cys Ile Pro Thr Leu His Ser Ile Phe His Pro Pro Pro  
 50 55 60  
 Thr Ser Arg Arg Ile Val Pro Arg Ala Val Phe Leu Gln Gly Val Arg  
 65 70 75 80  
 Gly Ile Thr His Ser Trp Arg Leu Ala Arg Arg Gln Ser Glu Ala Arg  
 85 90 95  
 Asp Thr

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 791 base pairs  
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

```

CTCCTCTGTC CACTGCTTTC GTGAAGACAA GATGAAGTTC ACAATTGTCT TTGCTGGACT 60
TCTTGGAGTC TTTCTAGTTC CTGCCCTAGC TAACATAAAT ATCAACGTCA ATGATGACAA 120
CAACAATGCT GGAAGTGGGC AGCAGTCAGT GAGTGTCAAC AATGAACACA ATGTGGCCAA 180
TGTTGACAAT AACACGGAT GGGACTCCTG GAATGCCATC TGGGATTATG GAAATGGCTT 240
TGCTGCAACC AGACTCTTTC AAAAAGAGAC ATGCATTGTG CACAAAATGA ACAAGGAAGT 300
CATGCCCTCC ATTCAATCCC TTGATGCACT GGTCAAGGAA AAGAAGCTTC AGGGTAAGGG 360
ACCAGGAGGA CCACCTCCCA AGGGCCTGAT GTACTCAGTC AACCCAAACA AAGTCGATGA 420
CCTGAGCAAG TTCGAAAAAA ACATTGCAAA CATGTGTCGT GGGATTCCAA CATACATGGC 480
TGAGGAGATT CAAGAGGCAA GCCTGTTTTT TTACTCAGGA ACGTGCTACA CGACCAGTGT 540
ACTATGGATT GTGGACATTT CCTTCTGTGG AGACACGGTG GAGAACTAAA CAAATTTTTA 600
AAGCCCATAT GGATTTAGTC ATCTGAATAT GCTGTGCAGA AAAAAATATGG GCTCCAGTGG 660
TTTTTACCAT GTCATTCTGA AATTTTTTCT TACTAGTTAT GTTTGATTTC TTTAAGTTTC 720
AATAAAATCA TTTAGCCTTG AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 780
AAAAAAAAAA A 791

```

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 185 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

```

Met Lys Phe Thr Ile Val Phe Ala Gly Leu Leu Gly Val Phe Leu Ala
 1             5             10             15

Pro Ala Leu Ala Asn Tyr Asn Ile Asn Val Asn Asp Asp Asn Asn Asn
20             25             30

Ala Gly Ser Gly Gln Gln Ser Val Ser Val Asn Asn Glu His Asn Val
35             40             45

Ala Asn Val Asp Asn Asn Asn Gly Trp Asp Ser Trp Asn Ser Ile Trp
50             55             60

Asp Tyr Gly Asn Gly Phe Ala Ala Thr Arg Leu Phe Gln Lys Lys Thr
65             70             75             80

Cys Ile Val His Lys Met Asn Lys Glu Val Met Pro Ser Ile Gln Ser
85             90             95

Leu Asp Ala Leu Val Lys Lys Lys Leu Gln Gly Lys Gly Pro Gly
100            105            110

```



Gly Pro Pro Lys Gly Leu Met Tyr Ser Val Asn Pro Asn Lys Val  
115 120 125

Asp Asp Leu Ser Lys Phe Gly Lys Asn Ile Ala Asn Met Cys Arg Gly  
130 135 140

Ile Pro Thr Tyr Met Ala Glu Glu Met Gln Glu Ala Ser Leu Phe Phe  
145 150 155 160

Tyr Ser Gly Thr Cys Tyr Thr Thr Ser Val Leu Trp Ile Val Asp Ile  
165 170 175

Ser Phe Cys Gly Asp Thr Val Glu Asn  
180 185

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2012 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

CTCAAGTTCA TCATTGTCCT GAGAGAGAG AGCAGCGCGG TTCTCGGCCG GGACAGCAGA 60  
ACGCCAGGGG ACCCTCACCT GGGCGCGCGG GGGCAGCGGC TTTGATTGTC CTGGGGTCGC 120  
GGAGACCCCG GCGCCTGCCC TGCACGCGCG GCGGCAACCT TTGCAGTCGC GTTGGCTGCT 180  
CGCATCGGCC GCGGGGTCCC TGCCGAAGGC TCGGCTGCTT CTGTCCACCT CTTACACTTC 240  
TTCAATTATC GTGGATCAT TTCGAGATC CGTCTTGTA ATGTTTGGA CTTTGCTACT 300  
TTATTGCTTC TTTCTGGCGA CAGTTCACGC ACTCGCCGAG ACCGCGGGAG AAAGGCAGCT 360  
GAGCCCGGAG AAGAGCGAAA TATGGGGACC CGGGCTAAAA GCAGACGTCG TCCTTCCCCC 420  
CCGCTATTTC TATATTCAAG CAGTGGATAC ATCAGGGAAT AAATTCACAT CTTCTCCAGC 480  
CGAAAAGGTC TTCCAGGTGA AAGTCTCAGC ACCAGAGGAG CAATTCACTA GAGTTGGAGT 540  
CCAGGTTTTA GACCGAAAAG ATGGGTCCCT CATAGTAAGA TACAGAATGT ATGCAAGCTA 600  
CAAAATCTG AAGGTGGAAA TTAATTTCCA AGGGCAACAT GTGGCCAAAT CCCCATATAT 660  
TTTAAAGGG CCGGTTTACC ATGAGAACTG TGACTGTCT CTGCAAGATA GTGCAGCCTG 720  
GCTACGGGAG ATGAAGTCCC CTGAAACCAT TGCTCAGATT CAGAGAGATC TGGCACAATT 780  
CCCTGCTGTG GATCCAGAAA AGATTGCAGT AGAAATCCCA AAAAGATTTG GACAGAGGCA 840  
GAGCCTATGT CACTACACCT TAAAGGATA CAAGGTTTAT ATCAAGACTC ATGGTGAAC 900  
TGTAGGTTT AGAATTTTCA TGGATGCCAT ACTACTTTCT TTGACTAGAA AGGTGAAGAT 960  
CCGAGATGTG GAGCTCTTTG TTAATTTGGG AGACTGGCCT TTGGAAAAAA AGAAATCCAA 1020  
TTCAAACATC CATCCGATCT TTTCTGGTGT TGGCTCCACA GATTCCAAGG ATATCTGTAT 1080  
GCCTACGTAC GATTGACTG ATTCTGTCTT GGAAACCATG GCGCGGGTAA GTCTGGATAT 1140  
GATGTCCTGT CAAGCTAACA CCGGTCTCCC CTGGGAAAGC AAAAATTTCA CTGCGTCTGT 1200  
GAGAGGGCGA GACAGCCGCA AAGAGAGACT CGAGCTGGTT AAACCTCAGT AAAACACACC 1260  
AGAATCATTA GACGCTGCTT TCACCAACTT TTTCTCTTT AAACAGGATG AAAACCTGTA 1320  
TGGTCCCAT GTGAACATA TTTCAATTTT TGATTCTCT AAGCATAAAT ATCAATAA 1380  
TATCGATGAG ACTGTAGCAG CTTATCGCCT GCCATATTG CTAGTTGGTG ACAGTGTGTT 1440  
GCTGAAGCAG GATTCCATCT ACTATGAACA TTTTACAAT GAGCTGCAGC CCTGGAAACA 1500  
CTACATTTCA GTTAAGACCA ACCTGAGCGA TCTGCTAGAA AAACCTTAAAT GGGCGAAAGA 1560  
TCACGATGAA GAGGCGAAAA AGATAGCAAA AGCAGGACAA GAAATTTGCA GAAATATCT 1620  
CATGGGCGAT GACATATTCT GTTATTATTT CAACTYTTT CAGGAATATG CCAATTTACA 1680

AGTGAGTGTAG CCCCAAATCC GAGAGGGCAT GAMAAGGGTA GAACCACAGA CTGAGGACGA 1740  
 CCTCTTCCST TGTAATTGCC ATAGGAAAAA GACCAAAGAT GAACSTGTAT ATGCAAAATA 1800  
 ACTTCTATTA GAATAATGGT GCTCTGAAGA CTCTTCTTAA CTAAAAAGAA GAATTTTTTT 1860  
 AAGTATTAT TCCATGGACA ATATAAAATC TGTGTGATTG TTTGCAGTAT GAAGACACAT 1920  
 TTCTACTTAT GCAGTATTCT CATGACTGTA CTITAAAGTA CATTTTTAGA ATTTTATAAT 1980  
 AAAACCACCT TTATTTTAAA AAAAAAAAAA AA 2012

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Met	Phe	Gly	Thr	Leu	Leu	Tyr	Cys	Phe	Phe	Leu	Ala	Thr	Val	Pro	1	5	10	15
Ala	Leu	Ala	Glu	Thr	Gly	Gly	Glu	Arg	Gln	Leu	Ser	Pro	Glu	Lys	Ser	20	25	30
Glu	Ile	Trp	Gly	Pro	Gly	Leu	Lys	Ala	Asp	Val	Val	Leu	Pro	Ala	Arg	35	40	45
Tyr	Phe	Tyr	Ile	Gln	Ala	Val	Asp	Thr	Ser	Gly	Asn	Lys	Phe	Thr	Ser	50	55	60
Ser	Pro	Gly	Glu	Lys	Val	Phe	Gln	Val	Lys	Val	Ser	Ala	Pro	Glu	Glu	65	70	75
Gln	Phe	Thr	Arg	Val	Gly	Val	Gln	Val	Leu	Asp	Arg	Lys	Asp	Gly	Ser	85	90	95
Phe	Ile	Val	Arg	Tyr	Arg	Met	Tyr	Ala	Ser	Tyr	Lys	Asn	Leu	Lys	Val	100	105	110
Glu	Ile	Lys	Phe	Gln	Gly	Gln	His	Val	Ala	Lys	Ser	Pro	Tyr	Ile	Leu	115	120	125
Lys	Gly	Pro	Val	Tyr	His	Glu	Asn	Cys	Asp	Cys	Pro	Leu	Gln	Asp	Ser	130	135	140
Ala	Ala	Trp	Leu	Arg	Glu	Met	Asn	Cys	Pro	Glu	Thr	Ile	Ala	Gln	Ile	145	150	155
Gln	Arg	Asp	Leu	Ala	His	Phe	Pro	Ala	Val	Asp	Pro	Glu	Lys	Ile	Ala	165	170	175
Val	Glu	Ile	Pro	Lys	Arg	Phe	Gly	Gln	Arg	Gln	Ser	Leu	Cys	His	Tyr	180	185	190
Thr	Leu	Lys	Asp	Asn	Lys	Val	Tyr	Ile	Lys	Thr	His	Gly	Glu	His	Val			

195										200										205													
Gly	Phe	Arg	Ile	Phe	Met	Asp	Ala	Ile	Leu	Leu	Ser	Leu	Thr	Arg	Lys																		
	210						215					220																					
Val	Lys	Met	Pro	Asp	Val	Glu	Leu	Phe	Val	Asn	Leu	Gly	Asp	Trp	Pro																		
225					230					235					240																		
Leu	Glu	Lys	Lys	Lys	Ser	Asn	Ser	Asn	Ile	His	Pro	Ile	Phe	Ser	Trp																		
				245					250					255																			
Cys	Gly	Ser	Thr	Asp	Ser	Lys	Asp	Ile	Val	Met	Pro	Thr	Tyr	Asp	Leu																		
			260					265						270																			
Thr	Asp	Ser	Val	Leu	Glu	Thr	Met	Gly	Arg	Val	Ser	Leu	Asp	Met	Met																		
			275				280						285																				
Ser	Val	Gln	Ala	Asn	Thr	Gly	Pro	Pro	Trp	Glu	Ser	Lys	Asn	Ser	Thr																		
290						295					300																						
Ala	Val	Trp	Arg	Gly	Arg	Asp	Ser	Arg	Lys	Glu	Arg	Leu	Glu	Leu	Val																		
305					310					315					320																		
Lys	Leu	Ser	Arg	Lys	His	Pro	Glu	Leu	Ile	Asp	Ala	Ala	Phe	Thr	Asn																		
				325					330					335																			
Phe	Phe	Phe	Phe	Lys	Gln	Asp	Glu	Asn	Leu	Tyr	Gly	Pro	Ile	Val	Lys																		
			340					345					350																				
His	Ile	Ser	Phe	Phe	Asp	Phe	Phe	Lys	His	Lys	Tyr	Gln	Ile	Asn	Ile																		
		355				360					365																						
Asp	Gly	Thr	Val	Ala	Ala	Tyr	Arg	Leu	Pro	Tyr	Leu	Leu	Val	Gly	Asp																		
	370					375					380																						
Ser	Val	Val	Leu	Lys	Gln	Asp	Ser	Ile	Tyr	Tyr	Glu	His	Phe	Tyr	Asn																		
385					390					395				400																			
Glu	Leu	Gln	Pro	Trp	Lys	His	Tyr	Ile	Pro	Val	Lys	Ser	Asn	Leu	Ser																		
				405					410					415																			
Asp	Leu	Leu	Glu	Lys	Leu	Lys	Trp	Ala	Lys	Asp	His	Asp	Glu	Glu	Ala																		
		420						425					430																				
Lys	Lys	Ile	Ala	Lys	Ala	Gly	Gln	Glu	Phe	Ala	Arg	Asn	Asn	Leu	Met																		
		435					440					445																					
Gly	Asp	Asp	Ile	Phe	Cys	Tyr	Tyr	Phe	Lys	Leu	Phe	Gln	Glu	Tyr	Ala																		
	450					455					460																						
Asn	Leu	Gln	Val	Ser	Glu	Pro	Gln	Ile	Arg	Glu	Gly	Met	Xaa	Arg	Val																		
465					470					475				480																			
Glu	Pro	Gln	Thr	Glu	Asp	Asp	Leu	Phe	Xaa	Cys	Thr	Cys	His	Arg	Lys																		
				485				490					495																				
Lys	Thr	Lys	Asp	Glu	Leu																												

## (2) INFORMATION FOR SEQ ID NO:149:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

GNAAGAAGAG AGCAACAGCC AGGACCAAG

29

## (2) INFORMATION FOR SEQ ID NO:150:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

CNCAGGCTAG GCACTGATTC TGCTGGTTC

29

## (2) INFORMATION FOR SEQ ID NO:151:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

GNAGACATGA AAGTTGAGCA GAAGGAAAG

29

## (2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:  
 GNGGTGCTTT TGATATCCAG CCATCTCTA 29

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 29 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:  
 CNTGGAAAGA GGAGCAAGAA CCAAGGCAG 29

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 29 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:  
 TNGGTTTTGT ACGTTGTGCT CTTTCATC 29

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 29 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:  
 TNATGGTCTA TATAACTGTC CTCCTTCCT 29

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 29 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

CNACACTGGG TCTCAGATCC TTCTGCTGA 29

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

GNCTCCAAGA AGTCCAGCAA AGACAATTG 29

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

ANTGCCAAAC ATTACAAGA CGGACTCTC 29

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1776 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

AGCTCACAGT AGCCCGGGGG CCCAGGGCAA TCCGACCACA TTCACTCTC ACCGCTGTAG 60

GAATCCAGAT GCAGGCCAAG TACAGCAGCA CGAGGGACAT GCTGGATGAT GATGGGGACA 120  
 CCACCATGAG CTTGCATTCT CAAGCCTCTG CCACAACTCG GCATCCAGAG CCCCAGCGCA 180  
 CAGAGCAGAG GGCTCCCTCT TCAACGTGGC GACCAGTGGC CCTGACCCTG CTGACTTTGT 240  
 GCTTGGTGCT GCTGATAGGG CTGGCAGCCC TGGGGGCTTT GTTTTTTCAG TACTACCAGC 300  
 TCTCCAATAC TGGTCAAGAC ACCATTTCTC AATGGGAAGA AAGATTAGGA AATACGTCCC 360  
 AAGAGTTGCA ATCTCTTCAA GTCCAGAATA TAAAGCTTGC AGGAAGTCTG CAGCATGTGG 420  
 CTGAAAAACT CTGTGCTGAG CTGTATAACA AAGCTGGAGC ACACAGGTGC AGCCCTTGTA 480  
 CAGAACATG GAAATGGCAT GGAGACAATT GCTACCAGTT CTATAAAGAC AGCAAAAAGTT 540  
 GGGAGGACTG TAAATATTTC TGCCCTTAGT AAAACTCTAC CATGCTGAAG ATAAACAAAC 600  
 AAGAAGACCT GGAATTTGCC GCGTCTCAGA GCTACTCTGA GTTTTTCTAC TCTTATTGGA 660  
 CAGGGCTTTT GGCCTCTGAC AGTGGCAAGG CCTGGCTGTG GATGGATGGA ACCCCTTTCA 720  
 CTTCTGAAC GTTCTCATAT ATAATAGATG TCACACAGCC AAGAAGCAGA GACTCTGTGG 780  
 CCATCCTTAA TGGGATGATC TTCTCAAAG ACTGCAAGA ATTGAAGCGT TGTGTCTGTG 840  
 AGAGAAGGGC AGGAATGGTG AAGCCAGAGA GCCTCCATGT CCCCCTGAA ACATTAGGCG 900  
 AAGGTGACTG ATTCGCCCTC TGCAACTACA AATAGCAGAG TGAGCCAGGC GGTGCCAAG 960  
 CAAGGGCTAG TTGAGACATT GGGAAATGGA ACATAATCAG GAAAGACTAT CTCTCTGACT 1020  
 AGTACAAGAT GGGTCTCTGT GTTTCCTGTT CAGGATCACC AGCATTTCTG AGCTTGGGTT 1080  
 TATGCACGTA TTAAACAGTC ACAAGAAGTC TTATTACAT GCCACCAACC AACCTCAGAA 1140  
 ACCCATAATG TCATCTGCCT TCTTGGCTTA GAGATAACTT TTAGCTCTCT TCTCTCTCAA 1200  
 TGTCTAATAT CACCTCCCTG TTTTCATGTC TTCTCTACAC TTGGTGGAAT AAGAAACTTT 1260  
 TTGAAGTAGA GGAAATACAT TGAGGTAAAC TCCTTTTCTC TGACAGTCAA GTAGTCCATC 1320  
 AGAAATTGGC AGTCACTTCC CAGATTGTAC CAGCAAAATC ACAAGGAATT TTTTTGTTT 1380  
 GTTTCAGTTC ATACTAGTCC CTTCCTCAAT CATCAGTAAA GACCCCATCT GCCTTGTTCA 1440  
 TGCCGTTTCC CAACAGGAT GTCACTTGAT ATGAGAATCT CAAATCTCAA TGCCTTATA 1500  
 GCATTCCTTC CTGTGTCCAT TAAGACTCTG ATAATTGTCT CCCCCTCATA GGAATTTCTC 1560  
 CCAGGAAAAA AATATATCCC CATCTCCGTT TCATATCAGA ACTACCGTCC CCGATATTCC 1620  
 TCTCAGAGAG ATTAAAGACC AGAAAAAAGT GAGCCTCTTC ATCTGCAGCT GTAAATGTTT 1680  
 CAGTTCCTAT TTCTTTCAT TGACCCATAT TTAATACCTT CAGGTACTGA AGATTATAA 1740  
 ATAATAAGT TAAATACGT GAAAAAATAA AAAAAA 1776

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

Met Gln Ala Lys Tyr Ser Ser Thr Arg Asp Met Leu Asp Asp Asp Gly  
 1 5 10 15  
 Asp Thr Thr Met Ser Leu His Ser Gln Ala Ser Ala Thr Thr Arg His  
 20 25 30  
 Pro Glu Pro Arg Arg Thr Glu His Arg Ala Pro Ser Ser Thr Trp Arg  
 35 40 45  
 Pro Val Ala Leu Thr Leu Thr Leu Cys Leu Val Leu Leu Ile Gly  
 50 55 60  
 Leu Ala Ala Leu Gly Leu Leu Phe Phe Gln Tyr Tyr Gln Leu Ser Asn

65	70	75	80
Thr Gly Gln Asp Thr Ile Ser Gln Met	Glu Glu Arg Leu Gly Asn Thr		
85	90	95	
Ser Gln Glu Leu Gln Ser Leu Gln Val	Gln Asn Ile Lys Leu Ala Gly		
100	105	110	
Ser Leu Gln His Val Ala Glu Lys Leu Cys Arg	Glu Leu Tyr Asn Lys		
115	120	125	
Ala Gly Ala His Arg Cys Ser Pro Cys Thr	Glu Gln Trp Lys Trp His		
130	135	140	
Gly Asp Asn Cys Tyr Gln Phe Tyr Lys Asp	Ser Lys Ser Trp Glu Asp		
145	150	155	160
Cys Lys Tyr Phe Cys Leu Ser Glu Asn Ser	Thr Met Leu Lys Ile Asn		
165	170	175	
Lys Gln Glu Asp Leu Glu Phe Ala Ala Ser	Gln Ser Tyr Ser Glu Phe		
180	185	190	
Phe Tyr Ser Tyr Trp Thr Gly Leu Leu Arg	Pro Asp Ser Gly Lys Ala		
195	200	205	
Trp Leu Trp Met Asp Gly Thr Pro Phe Thr	Ser Glu Leu Phe His Ile		
210	215	220	
Ile Ile Asp Val Thr Ser Pro Arg Ser Arg	Asp Cys Val Ala Ile Leu		
225	230	235	240
Asn Gly Met Ile Phe Ser Lys Asp Cys Lys	Glu Leu Lys Arg Cys Val		
245	250	255	
Cys Glu Arg Arg Ala Gly Met Val Lys Pro	Glu Ser Leu His Val Pro		
260	265	270	
Pro Glu Thr Leu Gly Glu Gly Asp			
275	280		

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 947 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

CAACTATCCC ATAATTTATT TATTCTTCTT CAATGTTTGT AAAGTGCATG AGTCATGTTT 60



ACACTTGAAG TCTAGTAGTG CACTGTAATA ATTCAATTTT TAAAAGATTA TTTAATGCCC 120  
 ATTTCAAAAT ACAGTAGITT ACACAGCTAC AGAAACAATT TGGGGCAAGT TTTAAACAC 180  
 TGAACACGTA ATAGTTATTG GTGTACACATA AAACCTGATT GTTTTTTACA GCCAAACCTC 240  
 TGTCAGTCAG AGGCATTCAT TAGTTTTATA CATGTAATTT GAAAATCACT AAACCTCGTT 300  
 TTCTCAGCAG CAATAATTTA AGAGGCTTCA AAAATATAAT TTCACTCTTA TTTAGTATTT 360  
 TTTCTGGGG GGATTTTAC GTAATTTTTT TATGAAAAGA CAAATGCATG TTGAGATAAC 420  
 TTCTGGGATT AAAATAGTCT TTTGCTTTAC TTTTGTGGTT TCCTAAAACA ACTTATTTGA 480  
 CTTTTAGTCC ATACTGTTAT ATTTTGTCT TAAAGAAAAT TTAACCTACA AATACCAAAA 540  
 GAAACATTT TAAATTTAGG GATGAGACTT TGGTGTATCG TGGGTCTAGG TTTAATGAAC 600  
 ACATCTGGGG TTAAGTTGGC ATTTCTTCAC ATCTCCACAC CCACACCAAC CATCACAGCC 660  
 CCCACCAAC CTCTCCCAA CCCCAAAAGC ATTGTCCAGG GATATAGATT TTACCAAAGG 720  
 CTTCCTGGGA AGACGAGGGA GCAACACTTT AGATTAAATG TGATCAGACT TTCCTATTAG 780  
 ATATGGCTCT TCTGTCTCTT GTTATCCCC TGACAGCTCT GCCATAAAGT CCCTCTCTCT 840  
 CATCTCTCCC AAACAGGCTG TATAAGTGCT TTGAGGTRAT TAACTCTTTT CCTCCAGTTT 900  
 ACAAAATATCA CTTAACAAAA AAAAAAAAAA AAAAAAAA 947

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Met Arg Leu Trp Cys Ile Val Gly Leu Gly Leu Met Asn Thr Ser Gly  
 1 5 10 15  
 Val Lys Leu Ala Phe Leu His Ile Ser Thr Pro Thr Pro Thr Ile Thr  
 20 25 30  
 Ala Pro His Gln Pro Ser Pro Asn Pro Lys Ser Ile Val Gln Gly Tyr  
 35 40 45  
 Arg Phe Tyr Gln Arg Leu Pro Gly Lys Thr Arg Glu Gln His Phe Arg  
 50 55 60  
 Leu Asn Val Ile Arg Leu Ser Tyr  
 65 70

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

CGCTGACTTG GGCAATGGGG CCGGTGGGGT TTGGGGCGG AAGAGACCCT CGGGTTGAG 60

AAGTATGTGG TGGCCTTTG TCCCTTGTA AACATTGTCA CACGGTGTGG GCGCGCAGCG 120  
 CTGGATCTTT GCAGGCTAT TTTGGCATT TCGTGGATAT ATGTTTCGTAA ATACCAAAGT 180  
 CCGCGGGAAA GTGAAGTTGT TCCACCATA ACAGCAATTT TTCTCTAGC AATTGCACCT 240  
 ATCACATCAG CACTTCTACC AGTGGATATA TTTTGGTTT CTTACATGAA AATCAAAAT 300  
 GGTACATTTA AGGACTGGGC TAATGCTAAT GTCAGCAGAC AGATTGAGGA CACTGTATTA 360  
 TACGGTTACT ATACTTTATA TTCTGTATA TTGTTCTGTG TGTTCTCTCTG GATCCCTTTT 420  
 GTCTACTTCT ATATATGAAGA AAGGATGAT GATGATACTA GTAAATGTAC TCAAAATAAA 480  
 ACGGCACTCA AGTATACITT GGGATTGTGT GTGATTGTG CACTGCTTCT TTTAGTTGGT 540  
 GCCTTTGTTT CATTTGAATG TCCCAATAAC AAAAATTCTA CAGAGTGGGA AAAAGTGAAG 600  
 TCCCTATTTG AAGAACTTGG AAGTAGTCAT GGTTTAGCTG CATTTGTCATT TTCTATCAGT 660  
 TCTCTGACCT TGATTGGAAT GTTGGCAGCT ATAACCTTACA CAGCCTATGG CATGCTCTGG 720  
 TTACCTTTAA ATCTGATAAA AGGCACCTAGA AGCGCTGCTT ATGAACGTTT GGAAACACAT 780  
 GAAGACATTG AAGAAGTAGA ACAACACATT TTAACAAAT TTGAAGAAAG GTTACGAACA 900  
 CGACCTTTGC CAGCAAGGGA TAAACGCGCC TTAACAAAT TTGAAGAAAG GTTACGAACA 960  
 CTTAAGAAAG GAGAGAGGCA TTTAGAATTC ATTTGAAACA GCTGGTGGAC AAAATTTTGT 960  
 GCGCTCTGCG GTCCCTTGAA GATCGCTGCG GGAATATTTT TCATCTTAGT TGCATTGCTG 1020  
 TTTGTAATTT CTCTTTTCIT GTCAAATTTA GATAAGGCTC TTCATTACAGC TGGAATAGAT 1080  
 TCTGGTTTCA TAATTTTTTG AGCTAACCTG AGTAATCCAC TGAATATGCT TTTGCTTTTA 1140  
 CTACAAACAG TTTTCCCTCT TGATTATATT CTTATAACAA TTATTATTAT GTACTTTATT 1200  
 TTTACTTCAA TGGCAGGAAT TCGAAATATT GGCATATGGT TCTTTGGAT TAGATTATAT 1260  
 AAAATCAGAA GAGGTAGAAC CAGGCCCCAA GCACCTCTTT TTCTCTGCAT GATACTTCTG 1320  
 CTTATTGTCC TTCACACTAG CTACATGATT TATAGTCTGT CTCCCCAATA TGTATATGAT 1380  
 GGAAGCCAAA ATTACTTAAT ASAGACTAAT ATAACITCTG ATAATCATAA AGGCAATTCA 1440  
 ACCCTTTCTG TGCCAAAGAG ATGTGATGCA GATGCTCCTG AAGATCAGTG TACTGTTACC 1500  
 CGGACATAACC TATTCCTTCA CAAGTTCTGG TTCTCTCAGT CTGCTTACTA TTTTGGTAAC 1560  
 TGGGCCITTC TTGGGGTATT TTTGATTGGA TTAATTGTAT TCGGTTGTAA AGGGAAGAAA 1620  
 TCGGTTATTG AAGGAGTAGA TGAAGATTG GACATAAGTG ATGATGAGCC CTCTGCTTAT 1680  
 TCTGCTTGAC AGCCTTCTGT CTTAAAGGTT TTATAATGCT GACTGTAATAT CTGTTATGCA 1740  
 TTTTAAAGT ATTAACTRA CATTAGGATT TGCTAACTAG CTTTTCATCAA AAATGGGAGC 1800  
 ATGGCTATAA GACAACTATA TTTTATTATA TGTTTTCTGA AGTAACATTG TATCATAGAT 1860  
 TAACATTTTA AATTACCATA ATCATGCTAT GTAAATATAA GACTACTGGC TTTTGGAGGG 1920  
 AATGTTTGTG CAAAATTTT TCCTCTAATG TATAATAGTG TTAATTTGAT TAAAAATCTT 1980  
 CCAGAATTAA TATTCCTTTT TGTCACTTTT TGAAACATA ATAAATCATT TGATCTCTGT 2040  
 CCTTAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2100  
 AAAAAAAAAA AAAAAAAAAA

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

Met Lys Asn Gln Asn Gly Thr Phe Lys Asp Trp Ala Asn Ala Asn Val  
 1 5 10 15  
 Ser Arg Gln Ile Glu Asp Thr Val Leu Tyr Gly Tyr Tyr Thr Leu Tyr  
 20 25 30  
 Ser Val Ile Leu Phe Cys Val Phe Phe Trp Ile Pro Phe Val Tyr Phe  
 35 40 45

Tyr Tyr Glu Glu Lys Asp Asp Asp Thr Ser Lys Cys Thr Gln Ile  
 50 55 60  
 Lys Thr Ala Leu Lys Tyr Thr Leu Gly Phe Val Val Ile Cys Ala Leu  
 65 70 75 80  
 Leu Leu Leu Val Gly Ala Phe Val Pro Leu Asn Val Pro Asn Asn Lys  
 85 90 95  
 Asn Ser Thr Glu Trp Glu Lys Val Lys Ser Leu Phe Glu Glu Leu Gly  
 100 105 110  
 Ser Ser His Gly Leu Ala Ala Leu Ser Phe Ser Ile Ser Ser Leu Thr  
 115 120 125  
 Leu Ile Gly Met Leu Ala Ala Ile Thr Tyr Thr Ala Tyr Gly Met Ser  
 130 135 140  
 Ala Leu Pro Leu Asn Leu Ile Lys Gly Thr Arg Ser Ala Ala Tyr Glu  
 145 150 155 160  
 Arg Leu Glu Asn Thr Glu Asp Ile Glu Glu Val Glu Gln His Ile Gln  
 165 170 175  
 Thr Ile Lys Ser Lys Ser Lys Asp Gly Arg Pro Leu Pro Ala Arg Asp  
 180 185 190  
 Lys Arg Ala Leu Lys Gln Phe Glu Glu Arg Leu Arg Thr Leu Lys Lys  
 195 200 205  
 Arg Glu Arg His Leu Glu Phe Ile Glu Asn Ser Trp Trp Thr Lys Phe  
 210 215 220  
 Cys Gly Ala Leu Arg Pro Leu Lys Ile Val Trp Gly Ile Phe Phe Ile  
 225 230 235 240  
 Leu Val Ala Leu Leu Phe Val Ile Ser Leu Phe Leu Ser Asn Leu Asp  
 245 250 255  
 Lys Ala Leu His Ser Ala Gly Ile Asp Ser Gly Phe Ile Ile Phe Gly  
 260 265 270  
 Ala Asn Leu Ser Asn Pro Leu Asn Met Leu Leu Pro Leu Leu Gln Thr  
 275 280 285  
 Val Phe Pro Leu Asp Tyr Ile Leu Ile Thr Ile Ile Ile Met Tyr Phe  
 290 295 300  
 Ile Phe Thr Ser Met Ala Gly Ile Arg Asn Ile Gly Ile Trp Phe Phe  
 305 310 315 320  
 Trp Ile Arg Leu Tyr Lys Ile Arg Arg Gly Arg Thr Arg Pro Gln Ala  
 325 330 335  
 Leu Leu Phe Leu Cys Met Ile Leu Leu Leu Ile Val Leu His Thr Ser  
 340 345 350

Tyr Met Ile Tyr Ser Leu Ala Pro Gln Tyr Val Met Tyr Gly Ser Gln  
355 360 365

Asn Tyr Leu Ile Glu Thr Asn Ile Thr Ser Asp Asn His Lys Gly Asn  
370 375 380

Ser Thr Leu Ser Val Pro Lys Arg Cys Asp Ala Asp Ala Pro Glu Asp  
385 390 395 400

Gln Cys Thr Val Thr Arg Thr Tyr Leu Phe Leu His Lys Phe Trp Phe  
405 410 415

Phe Ser Ala Ala Tyr Tyr Phe Gly Asn Trp Ala Phe Leu Gly Val Phe  
420 425 430

Leu Ile Gly Leu Ile Val Ser Cys Lys Gly Lys Lys Ser Val Ile  
435 440 445

Glu Gly Val Asp Glu Asp Ser Asp Ile Ser Asp Asp Glu Pro Ser Val  
450 455 460

Tyr Ser Ala  
465

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

GTTCGCAAAAT AAAAGATTTT GCAAAACCACT TTCCTACGTA CGTCCACTGT AGTTTTTGTCA 60  
GATACAACAC TAGCTGTAGC AAAGCCTATG TAAATCATAT GATGAGCTTT CATAGTAACC 120  
GTCCAAGCAA AAGGTTTTGT ATTTTAAAGA AGCATTGAGA AAATCTCCGG GGCATTACTC 180  
TAGTGTGCCT TAATTGTGAT TTCTTAAGTG ATGTTTCTGG CTTAGATAAT ATGGCTACAC 240  
ACTTAAGTCA ACATAAAACT CATACTTGCC AAGTTGTAAT GCAGAAAGTT TCTGTTTGTA 300  
TCCCAACTTC TGAGCACCTT TCTGAATTAA AAAAAGAAGC TCCCGCAAAG GAACAAGAAC 360  
CTGTGTCTAA GGAATTTGCA AGACCTAACA TGGCTGAAAG AGAAACAGAA ACATCAAAAT 420  
CTGAAAGTAA ACAAGATAAA GCTGCTTCTT CAAAAGAAAA AAATGGATGT AATGCAAAAT 480  
CATTGAAGG CTCATCAACA ACAAAAAGTG AAGAAGAGCAT AACAGTTTCA GATAAGGAAA 540  
ATGAAACCTG TCTTGACAGC CAGGAAACTG GCTCAAAAAA CATCGTCAGT TGTGATTCAA 600  
ATATTGGTGC AGATAAAGTG GAAAGAAAAA AACAAATACA ACACGTTTGT CAGGAAATGG 660  
AGTTGAAGAT GTGCCAAAGT TCAGAAAACA TAATCTTATC TGATCAGATT AAAGATCACA 720  
ACTCCAGTGA AGCCAGATTT TCTTCAAAGA ATATTAAGGA TTTGCGATTA GCATCAGATA 780  
ATGTAAGCAT TGCATAGTTT TTGAGAAAAA GACATGAACC TGAATCTGTT AGTTCGTAGT 840  
TTAGCGAGCA AGGCAGTATT CATTTGGAAC CTCTGACTCC ATCCGAGGTA CTTGAGTATG 900  
AAGCCACAGA GATTCTTCAG AAAGGTAGTG GTGATCCTTC AGCCAAGACT GATGAAGTAG 960  
TGTTCTGATCA AACAGATGAC ATTCCTGGAG GAAATAACCC TAGCACACAA GAGGCAACAG 1020  
TAGACCTGGA AGATGAAAAA GAAAGAAGTT GAAATTAGTC ATTTTAAGTT TCAGTGTACC 1080

AACGATAAGG GCATTGGAA CAGTGCTATC AGGTGAGCTC AGTGGTGTCTG TTGTAGGTTC 1140  
AGAAATGGAA ATATGTGAAG GAGGTCACAC ATACACTTTA CCTGTATGTT CAACCTATGT 1200  
TATCAAAACAA ATCAATTCCAC CAATAATAGC ATGATTAGTA GGGATTCCCA AAAAGTTTTT 1260  
AAAAACACGA ACAGGATTTT AATGATAATT AAATTTGCGA TGGAAAGGTC TCATTTAATG 1320  
GTTTTCAGG AAATGGGATT TGGTTGCTGA CATGAATTGA TGATATTAGT AATATTTATA 1380  
AAGCCTTTCA AACCTCCATC AATCCTAAGC TAAAAATCTT TATTACCTGT ATATCCTTTT 1440  
CAGTTAACTG AGAGGAAGGG ATTTGGAAAC CATGTACTTT TGGGGAGTAA TTGATTAAAA 1500  
ACAATGGCTT ATTGGCATTG TTAATGAAGG CTTTATTTGT GAGGATGATG CTGGTAAATG 1560  
GAGCATGCTT AGAGTACTAA ATTGATCTAA TGAGAATTTG GATGAACATA AACTTAAATT 1620  
TGGATTTAAT ATAACATTCC AGTCAGAGCG ATGTAACAGC AATATTTGAA TCTTTGTACC 1680  
TCCATACAGG TGTTAGCCTG CCAGGCGTGA AGCTTACCTT AATTAAACTT TCAGTGAAGA 1740  
TGGAATTATT AAGATAATAA TTTATATTTG TGCTTTTTGT CAGTGTGTAA CGTGTGTAGA 1800  
AATTCCTTGA TGTATTAGTT GTATTAATGT AAAGTAGAAA CCCATCTGTT AACTCTCTGT 1860  
AGCTATTATG CTTTAAATAT TGTTTTAATG ATCTTCCTTA GAAATAGGCC CATAAAAATG 1920  
GTCTGGAAGC CAACCAAAAG TATGGTATAA TGTAGATATT GTAAAGCAGT AAACGAAAA 1980  
CATGTCCTGG CATGTATTCA GCCATGTTA AGTGACTTTT CTGTAATTGT AAAATAAAAA 2040  
CTTCAAAATG GACCTAAAAAC AGTGATGTAA AAGAAGCTGGT TTTGGAAATT TAGCCTAATT 2100  
TATCTATAAG ATGGCTGCTA AATTGATTTT TCAGTTCTTT TATCATCTA GAATATAATA 2160  
GATATAGAAA TGAATAATAT GAAGAACAGT AGTTTGCTTT GAAATACTAA TAACTTTTA 2220  
TTTAAAAATG TTCATTTTTA CTTCTTAAAA TGTGCTTTGG ATTCTTAAAT TTTGTTTAC 2280  
TGAATGTCCA ATGTTTTAAA TGGCGATTAA AATACTCTGC TGTATATAGT AGTTTTTGAG 2340  
TAAATATTG CAATAAAAAA CTGCCCCGA ATAAAAAAA AAAAAAAA AAAAAAAA 2400  
AAAAAAA AAAA AAAA AAAA AAAA AAAA AAAA AAAA 2460  
AAAAAAA AAAA AAAA AAAA AAAA AAAA AAAA AAAA 2487

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Met Met Ser Phe His Ser Asn Arg Pro Ser Lys Arg Phe Cys Ile Phe  
1 5 10 15  
Lys Lys His Ser Glu Asn Leu Arg Gly Ile Thr Leu Val Cys Leu Asn  
20 25 30  
Cys Asp Phe Leu Ser Asp Val Ser Gly Leu Asp Asn Met Ala Thr His  
35 40 45  
Leu Ser Gln His Lys Thr His Thr Cys Gln Val Val Met Gln Lys Val  
50 55 60  
Ser Val Cys Ile Pro Thr Ser Glu His Leu Ser Glu Leu Lys Lys Glu  
65 70 75 80  
Ala Pro Ala Lys Glu Gln Glu Pro Val Ser Lys Glu Ile Ala Arg Pro  
85 90 95

Asn Met Ala Glu Arg Glu Thr Glu Thr Ser Asn Ser Glu Ser Lys Gln  
 100 105 110  
 Asp Lys Ala Ala Ser Ser Lys Glu Lys Asn Gly Cys Asn Ala Asn Ser  
 115 120 125  
 Phe Glu Gly Ser Ser Thr Thr Lys Ser Glu Glu Ser Ile Thr Val Ser  
 130 135 140  
 Asp Lys Glu Asn Glu Thr Cys Leu Ala Asp Gln Glu Thr Gly Ser Lys  
 145 150 155 160  
 Asn Ile Val Ser Cys Asp Ser Asn Ile Gly Ala Asp Lys Val Glu Lys  
 165 170 175  
 Lys Lys Gln Ile Gln His Val Cys Gln Glu Met Glu Leu Lys Met Cys  
 180 185 190  
 Gln Ser Ser Glu Asn Ile Ile Leu Ser Asp Gln Ile Lys Asp His Asn  
 195 200 205  
 Ser Ser Glu Ala Arg Phe Ser Ser Lys Asn Ile Lys Asp Leu Arg Leu  
 210 215 220  
 Ala Ser Asp Asn Val Ser Ile Asp Gln Phe Leu Arg Lys Arg His Glu  
 225 230 235 240  
 Pro Glu Ser Val Ser Ser Asp Val Ser Glu Gln Gly Ser Ile His Leu  
 245 250 255  
 Glu Pro Leu Thr Pro Ser Glu Val Leu Glu Tyr Glu Ala Thr Glu Ile  
 260 265 270  
 Leu Gln Lys Gly Ser Gly Asp Pro Ser Ala Lys Thr Asp Glu Val Val  
 275 280 285  
 Ser Asp Gln Thr Asp Asp Ile Pro Gly Gly Asn Asn Pro Ser Thr Thr  
 290 295 300  
 Glu Ala Thr Val Asp Leu Glu Asp Glu Lys Glu Arg Ser  
 305 310 315

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

TTTATTTTTC	AAATCATAAT	TTTAAATGA	TAGATACCAT	TTTGTGATAA	CAACAATTCA	60
GAAACCAAT	TTCTATCCTC	TTAGTTGAAA	GAATGTAGGT	ACAGTTTGGG	TACTTGTACT	120
TTAATTTT	AGTAACATC	TGCATTATAC	TCTTATAGAT	AATGAAATTA	TTTAGTTAAG	180
AAATTCITTA	CAGTAAATGA	GATAATGTGT	GAAAAAGTAT	TTTGTAAATG	CTGAGGATTC	240
TACAATATGT	AGTTGTATT	TTTATGTGTA	TTTGTAAAGT	CATGTCCATT	TCATGAATAT	300
AGGACTTTC	ATAAAAAAG	ACTTCTCAA	GACAACTTTA	TATTTCTAGTA	TTTTCTGTGT	360
GTAAGAAATG	TTAACTATTT	ACTTTTATTT	TGTTATACAT	TTATTTTAAAT	ATCCATGTCT	420
TTATTATAGT	AAATTTGAAA	TGAAATCCTG	AAAAACAGAA	TTTTTTTAAA	CACAGAGGCT	480
ACACCAATAT	TAATTTTTTC	TCTACATAAT	TTAAAACTAC	ATAAATTAAAG	TACTTAAAAAT	540
TTATATTGAA	GGCCACCAG	AACTTAGGTT	GAATCTTAGA	AAATTTAAAT	AACTATTTTT	600
AAAGTTACCC	AACTTAATAT	TTTAAATTTT	TAATATTTAT	TTCTCCTTAC	TAACTCTTGA	660
TAATAATATG	CATTAGACTT	GATAAAATAA	AAAAGAATTT	TAGAGTAGAA	TTAATATATC	720
AAAAGGGGTA	TATCAACCAA	ATTGGTGTCA	GATTGTATTC	ATTCTCTCAT	CACATAAAGA	780
TTTTTCTTTT	GATAGGTGAT	GCTCATATGA	ACCTTTGGTT	TAGAATCTAT	ATATGTACAT	840
GTGTATGTAT	TGATAGTAGTA	TGGTGTGATA	CACACATATA	TACCAACAC	CATGAATTTT	900
AGCAGTCTGT	GATGATCAGC	AAAAAAGCAC	ATAAGATAAA	ATTAGTTGAC	CATGCTAAAT	960
CTCAATCTGG	AAITTTTTTT	TATTTGGGCA	TTTCTAGAAC	TTTTTACATT	TGAAAGTACA	1020
TGATGAGTAT	TAGTAAACGAT	GACTTATGTA	TAATCAGAAAT	CTTTATGACA	ATTAGTTTGT	1080
ACAAGGTCAG	AAGAGATGAG	TTTGCTAAAC	CCAGCTGTGA	TACCTCAGTT	GGAAAGGGAA	1140
TTCAAAGGTA	TGCTTTGTAG	AACGAAAAG	TATAGTTT	TTTTCAATGA	CTTAAATCT	1200
TTTCTGTTTT	TCTCTATGT	GAGTCAGTCA	CAAAAGTGGT	CTAATTTT	CAACAGTAGA	1260
ACTCTCTCCT	TTTCTACTGT	AATCTTCCCA	CTGACTTTAC	TGCAAGAGTA	TGAAATACTA	1320
GTGTATTGGA	TCTTCAGTAA	CCTTTTATAT	TCTAGATAGA	TTGAAATATA	GGATTTACTT	1380
CCATTAAAC	CAGGTGATAA	GATGATGTAA	ATACTCAGGG	AGGGTATTAA	CTTGTTACTT	1440
TTGCTCGTTT	GGGGTGTAAA	GTGCCATGAC	TGAATAATCT	TCAATTCATG	ATTCTAGAGT	1500
AAGTTTAAAT	TGGAAAAAGG	GGCTTCACAC	ATGGTGGTGG	TTGAACATTG	ATCTTTTTAT	1560
ACTTAAAAAG	ATGAAATGT	TTTGTGGACT	GATACATTTT	ATCTTACTGA	ATATGAATTG	1620
TTTATGTATC	TCTACTGTCA	AATAGCCTTT	TTGAAACTCA	GGAAAGACAA	AGGTTCAATT	1680
ACACCACTTT	TGTCATAAAG	CAAAACAGGT	ATTTTTTTTT	TCTCTTGTTG	TCTGGATATG	1740
GCAATAGATT	TTTTAAATTG	CTGTGAGAAC	CCATATATGA	AAAGAGAGGA	GTTGAATTGT	1800
GTGTGCTTTT	TATGTCTTGA	GATTTATATG	TGGAAGAGAC	GACATCTACT	TCAAACCTGA	1860
TTTTTTTCTG	TTTTTTTTTT	TTTTTGGGGA	AGGGGGGAGA	ACGGGGTCTT	GCTCTGTGCG	1920
CCAGGCTGGA	GTGCAGTGGC	GCATCTCAG	CTGACTGCAG	CCTCCACCTC	CCGGGTTCAA	1980
GGGATTCGCG	CTCAGCCTCC	CGAGTAGCTG	AGACCACAGG	TGCGTGCCAC	CACACCCGCG	2040
TAATTTTTTT	GTATTTTTAG	TAGAGACGGG	GTTTAGTAGA	GACGGATCAC	TCCTGACCAC	2100
GTGATCCGCG	CACCTCGGCG	TCCCAAAGTG	CTGGGATTAC	AGGCGTGAGC	CACCCCCCCC	2160
GGCCTGTATT	TTTCAGAGAG	AGAGCTTGGT	GTTTTTGGTG	TGCCAAGTGG	TAAGATAAATG	2220
TCTCTTTGAG	GCTTCTCTATG	GACTGCCTTT	ATTTTAGTAA	ACTCAAGACA	CCAGTTAAACC	2280
TCAACAGAGT	TTTGGCCCTTA	TAGAAATTTT	TTTGTGCATCT	TATTGAAAGC	CAGGTTTACA	2340
TCAACCTCAC	CCAATTATCT	TTTTAGTTAA	ATAAATTTAC	CATGCAAGGT	ACACAGAATG	2400
GATCAAAATTG	GTGTATCTTT	AAGGCAGTAG	GTTTGTACTAG	CTAGCTATCA	TTATTTGTAC	2460
ATCCTAATGCT	AGGCACCAGA	AACCATTTGA	GCCAGGAGTG	TGAATGAATA	ATTCCAGAG	2520
ACACTTTAGA	CATTTTTTAA	TGTTTTATAT	GACATTTTAC	ATTTGTGTGA	TGCGCTTGA	2580
TATTTAAATTT	TCTTAGTGCT	GATAAAAACA	GCAACATTTA	TAACTTATTT	TATATATTGT	2640
TCCAAAGAAA	AGAATTTGTT	TTAATGGTTT	CAAAATAACT	GACCTTGAAT	TTGTTTATGT	2700
GCCTTAAGTT	CTCTAGTGCT	ATTTCAACTT	TTTTTTCAAT	TAATAAGAG	CTTACCTTAG	2760
ATAAGGTTCA	TATTTGTGTT	CTATAGAGTA	AATAAACTTC	CCCTTCTTAA	ATTGTGTAAT	2820
AAGCACCAC	GTGTGGTTGC	TGGGCAGAA	GAGAATGTTA	AGGGAGATTG	TTGGATGTTT	2880
GGAGTTTCAT	TATATTTTTT	GTTTTTATTT	TTTGATACCT	AGGTGCTTTT	TAAATATTCT	2940
AGACAAATAT	CTATCTTACA	TTGATTTAAAC	CCGTGTAAAT	TCATTTGCG	TATCTACATC	3000
AAGTGTCAAA	AAAGTATACT	TATTTTTGTT	CCATACTTAT	GTACAAATTT	TTCCCTCTCT	3060
AGGCTTTTTT	ATTTACCTTT	TTGAAAAAGC	ACTTACTCTC	CCCTTCCCTA	TCACCCCTCC	3120
CCCAAGGTTT	CTTTATTTAA	ATTTTTATTG	AGAGTTGTTG	GAGCTCTAAG	ACAAATACAA	3180
TTTAGAGTTT	AACAAAGATA	TAATCTGCTT	TACAACTAGT	ATAGACCTAA	GGTCAITTCG	3240
TTTCAATTAG	AGGCTCCAGA	GTCTTCATAG	TGGAAGAAAT	GCTTTGTATT	TAATTTGTTCT	3300
TAGTTAAGTT	GTAGCACGTG	AATACTTACT	TACATGTTTT	GTTTAAATAT	ACTTCTTGCA	3360

TAGTTTAATT TTTTAAAGT TGTATCTAAT AAAATGTCTT TTAACCATTA TTAAGTACT 3420  
 ATATGGTTGT ATTAAATTTT GTTACGAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 3480  
 AAAAAAAAAA AAAAA 3495

(2) INFORMATION FOR SEQ ID NO:168:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 45 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Met Ser Lys Lys Tyr Thr Tyr Phe Cys Ser Ile Leu Met Tyr Asn Phe  
 1 5 10 15  
 Phe Pro Leu Gln Ala Phe Ser Phe Thr Phe Leu Lys Lys His Leu Leu  
 20 25 30  
 Ser Pro Ser Leu Ser Pro Leu Pro Gln Gly Phe Phe Ile  
 35 40 45

(2) INFORMATION FOR SEQ ID NO:169:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1398 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
 (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

GGTGTATCCAT CTGAGAAAGG GATCATGAAC TAGACAGAAT GAACAGCCTT AGAGGCACAG 60  
 ACTCTTGAAC GGGACGGTGG TGGTATGACT AGTGCAGAGT GTTTAGAGAT CACTCAGTTT 120  
 TTAAAGACTG GCCTTTATCG TGTCTCAGTG CAGCCGAGGC AGAGCCTTTG AAGGATGCGA 180  
 TGGTGTCTATT CTTACTAATC TAGTCCAGCC GCTGAGGTGA CTTTCAACGG CAGACCGTCT 240  
 CCTGAGCGCC CCAGGTAGAA TTTCAAAAGT CTCGGGACC ATTATGGCAG TCAAGTGGAC 300  
 GGGTGGGCAT TCTTCTCGTG TCCTCTGCCT GAATGCAAGT AAAGAAGGCG TGCTGGCTTC 360  
 TGGAGCAGAG GCGCGAGATC TCACGGCTTG GGGTGAAGAT GGAACCTCCAT TAGGACACAC 420  
 GCGGTTCCAA GGGGCTGATG ATGTTACCAG TGTCTTATTT TCTCCCTCCT GTCCACCAA 480  
 GCTCTATGCC TCACATGGAG AAACCATTAG TGTACTGGAT GTCAGGTCCC TCAAAGATTC 540  
 CTTGGACCAT TTTCATGTGA ATGAAGAAGA AATCAATTGT CTTTCATTGA ATCAACGGA 600  
 AAACCTGCTG GCTTCTGCTG ACGACTCTGG GGCAATCAAA ATCCTAGACT TGGAAAACAA 660  
 GAAAGTTATC AGATCCTTGA AGAGACATTC CAATATCTGC TCCTCAGTGG CTTTTCGGCC 720  
 TCAGAGGCCT CAGAGCCCTGG TGTCTATGCT ACTGGATATG CAGGTGATGC TGTGGAGTCT 780  
 TCAAAAGCCG CAGACACTCT GGATTACAAA TTTACAGGAG GATGAAACAG AAGAAATGGA 840  
 AGGCCACAG TCACCTGGTC AGCTCTTAAA CCCTGCCTTA GCCCATTTA TCTCTGTGGC 900



TTCGTGTGGT AATATTTTGA GTTGTGGTGC AGAAGATGGT AAGGTTTCGAA TCTTTCGGGT 960  
 GATGGGAGTT AAGTGTGAAC AGGAACTGGG ATTTAAGGGC CACACTTCAG GGGTATCCCA 1020  
 GGTCTGCTTT CTCCAGAAT CCTATTTGCT GCTTACTGGA GGGAAATGATG GGAAGATCAC 1080  
 GTTGTGGGAT GCAAAACAGTG AAGTTGAGAA AAAACAGAAAG AGTCCCAACA AACGTACCCA 1140  
 CAGGAAGAAA CCTAAAAGAG GAACTTGCAC CAAGCAGGGT GGAATATACTA ACGCTTCAGT 1200  
 AACAGATGAG GAAAGACATG GCAACATTTT ACCGAAGCTA AATATTGAAC ATGGAGAAAA 1260  
 AGTGAACCTG CTCTTGGGTA CAAAAATAAA GGGACACCAA AATATATTAG TAGCTGATCA 1320  
 AACTAGTTGT ATATCTGTAT ACCCCTTAAA TGAATTTTAA ATCCAATAAA AACATTTGAA 1380  
 GAAAAAATAA AAAAAAAA 1398

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

Met Ala Val Lys Trp Thr Gly Gly His Ser Ser Pro Val Leu Cys Leu  
 1 5 10 15  
 Asn Ala Ser Lys Glu Gly Leu Leu Ala Ser Gly Ala Glu Gly Gly Asp  
 20 25 30  
 Leu Thr Ala Trp Gly Glu Asp Gly Thr Pro Leu Gly His Thr Arg Phe  
 35 40 45  
 Gln Gly Ala Asp Asp Val Thr Ser Val Leu Phe Ser Pro Ser Cys Pro  
 50 55 60  
 Thr Lys Leu Tyr Ala Ser His Gly Glu Thr Ile Ser Val Leu Asp Val  
 65 70 75 80  
 Arg Ser Leu Lys Asp Ser Leu Asp His Phe His Val Asn Glu Glu Glu  
 85 90 95  
 Ile Asn Cys Leu Ser Leu Asn Gln Thr Glu Asn Leu Leu Ala Ser Ala  
 100 105 110  
 Asp Asp Ser Gly Ala Ile Lys Ile Leu Asp Leu Glu Asn Lys Lys Val  
 115 120 125  
 Ile Arg Ser Leu Lys Arg His Ser Asn Ile Cys Ser Ser Val Ala Phe  
 130 135 140  
 Arg Pro Gln Arg Pro Gln Ser Leu Val Ser Cys Gly Leu Asp Met Gln  
 145 150 155 160  
 Val Met Leu Trp Ser Leu Gln Lys Ala Arg Pro Leu Trp Ile Thr Asn  
 165 170 175  
 Leu Gln Glu Asp Glu Thr Glu Glu Met Glu Gly Pro Gln Ser Pro Gly

180 185 190

Gln Leu Leu Asn Pro Ala Leu Ala His Ser Ile Ser Val Ala Ser Cys  
195 200 205

Gly Asn Ile Phe Ser Cys Gly Ala Glu Asp Gly Lys Val Arg Ile Phe  
210 215 220

Arg Val Met Gly Val Lys Cys Glu Gln Glu Leu Gly Phe Lys Gly His  
225 230 235 240

Thr Ser Gly Val Ser Gln Val Cys Phe Leu Pro Glu Ser Tyr Leu Leu  
245 250 255

Leu Thr Gly Gly Asn Asp Gly Lys Ile Thr Leu Trp Asp Ala Asn Ser  
260 265 270

Glu Val Glu Lys Lys Gln Lys Ser Pro Thr Lys Arg Thr His Arg Lys  
275 280 285

Lys Pro Lys Arg Gly Thr Cys Thr Lys Gln Gly Gly Asn Thr Asn Ala  
290 295 300

Ser Val Thr Asp Glu Glu Glu His Gly Asn Ile Leu Pro Lys Leu Asn  
305 310 315 320

Ile Glu His Gly Glu Lys Val Asn Trp Leu Leu Gly Thr Lys Ile Lys  
325 330 335

Gly His Gln Asn Ile Leu Val Ala Asp Gln Thr Ser Cys Ile Ser Val  
340 345 350

Tyr Pro Leu Asn Glu Phe  
355

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

CCGAGAGTAG CTACCACGGC CTGTGTCAAC GACTAAAGCT CCAGTACAGC GGC GCCCTCA 60  
GACAGCTGGG AGGGTGGCTC TGGCCGGGAG CGGCGGCCGG TGAGCTACCG CGAGGAGGAG 120  
CGGCGGAGGC GACCTCGGCC CGGCCCTGCA CTGGCCGCCCG GGCAGGC GCGC ACATGAGCCT 180  
GGTCTGGCAT CCGCGGGATG CTCCTTAAGC CCCTTCTCCG GCTGTTAACC TCCGGGAAC 240  
GGTTGTGACC ACACCGACAC GTATTTTACA GATAAATCAT TCTTGCGGCG GCGGGTCGAA 300  
CACGTTTATT TATTTTAT TTTCTCAACA AGCTTTTACC CAGCACCTGT CCAGTGAAAC 360  
AACTTGATAA TCGTTTCGAG GGGCGTCCGC CGGGTTAGGA AGCCACTGCC TGGCAGCTTG 420  
TGAAGCCCTC ATTTGCAAG CCACCCCTCA GATGTTTGA AGATCGTGAC GTCTTGTAAC 480

TAGCAGTGTG TGCACAGAAT CCTACTCAAG GAACGTCTTG GCCCAGCGAT GCAAAGAAGT 540  
 GAAGTTTCAA GCTGGAAGAG CCTGTATTGT CCTCACAATA GTATAGAAGA ATTCAGAAGA 600  
 GGAGAGAGAG ACAGCACCGA ATGAAGACTG TAAAGAAAAA GAAGGAATGC CAGAGATTGA 660  
 GAAATCTGCG CAAGACTTAG AGGGTAACCC AGAGGAAACC GTCTTCAGGG CCTGTTTGCT 720  
 GGCTATGCGT TCGAGAACCT GGGGATCCCG AAAAAATTAGG GGAATTTCTT CAGAAAGACA 780  
 ATATCAGCGT GCATTATTTC TGCTTATCT TATCTAGTAA GCTGCCTCAG AGGGGCCAGT 840  
 CCAACAGAGG TTTCATGGA TTTCTGCCTG AAGACATCAA AAAGGAGGCA GCCCGGCTT 900  
 CTAGGAAGAT CTGCTTTGTG TGCAAGAAAA AGGGAGCTGC TATCAACTGC CAGAAGGATC 960  
 AGTGCCTCAG AAACCTTCCAT CTGCCCTTGTG GCCAAGAAAG GGGTTGCCTT TCACAAATTT 1020  
 TTGGAGAGTA CAAATCATTT TGTGACAAAC ATCGCCCAAC ACAGAACATC CAACATGGGC 1080  
 ATGTGGGGGA GGAAGACTGC ATCTTATGTT GTGAAGACTT ATCCCAACAG AGTGTGAGA 1140  
 ACATCCAGAG CCGGTGTTGT AGTCAAGCCA TCTACCACCG CAAGTGCGATA CAGAAATATG 1200  
 CCCACACATC AGCAAGACAT TTCTTCAAAT GTCCACAGTG TAACAATCGA AAAGAGTTTC 1260  
 CTCGAAGAAAT GCTGAGAATG GGAATTCATA TTCCAGACAG AGATGCTGCC TGGGAACCTG 1320  
 AGCCAGGGGC TTTCTCAGAC TTATATCAGC GCTATCAGCA CTGTGATGCC CCCATCTGTG 1380  
 CGTATGAACA AGGCAGAGAC AGCTTTGAGG ATGAAGGGAG GTGGTGCCTC ATTCTGTGTG 1440  
 CTACATCGCG ATCCACAGGA ACCCACAGGG ACTGCTCCTC TCTTAGATT AACAGTAAGA 1500  
 AATGGGAGTG TGAGGAGTGT TCACCTGCTG CAGCCACAGA CTACATACCT GAAAACTCAG 1560  
 GGGACATCCC TTGCTGCAGC AGCACCTTCC ACCCTGAGGA ACATTCTGTC AGAGACAACA 1620  
 CCTTGGAAGA GAATCCGGGC CTTTCTTGGA CTGATTGGCC AGAACCTTCC TTATTAGAAA 1680  
 AGCCAGAGTC CTCTCGTGGC AGGAGGAGCT ACTCCTGGAG GTCCAAGGCT GTCAGAATCA 1740  
 CTAACAGCTG CAAAAAATCC AAGTAACACC TTCTGAGTAG CTGCTGTCCC ACACAATAGG 1800  
 GTATGAAGCT GCGCTCCTCC ATCGGGTTTG GGGAGGGAGC ACTCTGGGAC TGTGAGACAA 1860  
 GGAAGCAGGG CCAGCAGTGA GACTATGAGC CAAGCAAAGA GAAGTCTCAG TGGAGCATGA 1920  
 GGAGGGAGCA GTCCAGATGC CAACAAGGAA ATGCGTTTTT GGCTACAAGA GTGCCTCTGC 1980  
 TTTCTCTCTC TCTCTCCCA CCAAGGATTC TTCCACCTTA ATCTTGTGTT CATATGCTCT 2040  
 TTCTTACTTC ACCCATGTT GTTGTATATG AAATAAAGGT TTTCTCTCCC AAAAAAATAA 2100  
 AAAAAAATAA AAAAAAATAA AAAAAAATAA AA 2132

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Met Lys Thr Val Lys Glu Lys Lys Glu Cys Gln Arg Leu Arg Lys Ser  
 1 5 10 15  
 Ala Lys Thr Arg Arg Val Thr Gln Arg Lys Pro Ser Ser Gly Pro Val  
 20 25 30  
 Cys Trp Leu Cys Leu Arg Glu Pro Gly Asp Pro Glu Lys Leu Gly Glu  
 35 40 45  
 Phe Leu Gln Lys Asp Asn Ile Ser Val His Tyr Phe Cys Leu Ile Leu  
 50 55 60  
 Ser Ser Lys Leu Pro Gln Arg Gly Gln Ser Asn Arg Gly Phe His Gly  
 65 70 75 80  
 Phe Leu Pro Glu Asp Ile Lys Lys Glu Ala Ala Arg Ala Ser Arg Lys

85										90										95													
Ile	Cys	Phe	Val	Cys	Lys	Lys	Lys	Gly	Ala	Ala	Ile	Asn	Cys	Gln	Lys																		
			100					105					110																				
Asp	Gln	Cys	Leu	Arg	Asn	Phe	His	Leu	Pro	Cys	Gly	Gln	Glu	Arg	Gly																		
			115				120					125																					
Cys	Leu	Ser	Gln	Phe	Phe	Gly	Glu	Tyr	Lys	Ser	Phe	Cys	Asp	Lys	His																		
			130			135					140																						
Arg	Pro	Thr	Gln	Asn	Ile	Gln	His	Gly	His	Val	Gly	Glu	Glu	Ser	Cys																		
					150					155					160																		
Ile	Leu	Cys	Cys	Glu	Asp	Leu	Ser	Gln	Gln	Ser	Val	Glu	Asn	Ile	Gln																		
				165				170					175																				
Ser	Pro	Cys	Cys	Ser	Gln	Ala	Ile	Tyr	His	Arg	Lys	Cys	Ile	Gln	Lys																		
			180				185						190																				
Tyr	Ala	His	Thr	Ser	Ala	Lys	His	Phe	Phe	Lys	Cys	Pro	Gln	Cys	Asn																		
			195			200						205																					
Asn	Arg	Lys	Glu	Phe	Pro	Gln	Glu	Met	Leu	Arg	Met	Gly	Ile	His	Ile																		
			210			215					220																						
Pro	Asp	Arg	Asp	Ala	Ala	Trp	Glu	Leu	Glu	Pro	Gly	Ala	Phe	Ser	Asp																		
			225		230				235					240																			
Leu	Tyr	Gln	Arg	Tyr	Gln	His	Cys	Asp	Ala	Pro	Ile	Cys	Pro	Tyr	Glu																		
				245				250					255																				
Gln	Gly	Arg	Asp	Ser	Phe	Glu	Asp	Glu	Gly	Arg	Trp	Cys	Leu	Ile	Leu																		
			260				265						270																				
Cys	Ala	Thr	Cys	Gly	Ser	His	Gly	Thr	His	Arg	Asp	Cys	Ser	Ser	Leu																		
			275			280					285																						
Arg	Phe	Asn	Ser	Lys	Lys	Trp	Glu	Cys	Glu	Glu	Cys	Ser	Pro	Ala	Ala																		
			290			295					300																						
Ala	Thr	Asp	Tyr	Ile	Pro	Glu	Asn	Ser	Gly	Asp	Ile	Pro	Cys	Cys	Ser																		
			305		310				315					320																			
Ser	Thr	Phe	His	Pro	Glu	Glu	His	Phe	Cys	Arg	Asp	Asn	Thr	Leu	Glu																		
				325				330					335																				
Glu	Asn	Pro	Gly	Leu	Ser	Trp	Thr	Asp	Trp	Pro	Glu	Pro	Ser	Leu	Leu																		
			340			345						350																					
Glu	Lys	Pro	Glu	Ser	Ser	Arg	Gly	Arg	Arg	Ser	Tyr	Ser	Trp	Arg	Ser																		
			355			360					365																						
Lys	Gly	Val	Arg	Ile	Thr	Asn	Ser	Cys	Lys	Lys	Ser	Lys																					
			370			375					380																						

(2) INFORMATION FOR SEQ ID NO:173:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 984 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid  
 (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

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GTCACGTGGA ACCTCTTAAT CTCAGCATCC GGAGCTCCAG GAAGGGAAAA TTTCAGTCA 60
GATAGAATTC TATATATACC ATTTCTTTGG AACCTTCAGC CCTCAAGATT CCAACATCAT 120
GACCTCAGTT TCAACACAGT TGTCCCTTAG CCTCATGTCA CTGCTTTTGG TGCTGCCTGT 180
TGTGGAAGCA GTAGAAGCCG GTGATGCAAT CGCCCTTTTG TTAGGTGTGG TTCTCAGCAT 240
TACAGGCATT TGTGCCTGCT TGGGGGTATA TGCACGAAAA AGAAATGGAC AGATGTGACT 300
TTGAAAGGCC TACTGAGTCA AACCTCACCC TGAAAACCTT TGCCTTTAG AGGCTAAACC 360
TGAGATTGGS TGTGTGAAG GTTCCAAGAA TCAGTAAATA AGGGAGTTTC ACATTTTTC 420
TTGTTTCCAT GAAATGGCAA CAAACATACA TTTATAAATT GAAAAAATA TGTTTTCTTT 480
ACAACAAATA ATGCACAGAA AAATGCAGCC TATAATTTGC TAGTTAGGTA GTCAAAGAAG 540
TAAGATGGCT GAAATTTACA TAAGTAATAT TTCATAATCT TAGAATTCCT TCAAAGCATG 600
TGAAATAGGA AGAAGGAAGT TCTTGCCCGA AATCCTTAGGA AATCACCCT GTTCGGTTAT 660
AATCACTGCC TCCTGAATCG TTGAGGAGTC TTTTAAATTA GATTTTGTGT TTGTGTGCTC 720
CCAAGTTAAT ATTTATTTTA GATATCAGAG AGTCAGGCCAA AAAGGAAAAAC TTTTATCTCT 780
AGGGAAAAAA CATTTAGAAA AATGTATTCA GTGTATCTAA TACTGAAATG CGGAAAAAAA 840
TTTAATGTTA AAAAAAAATC ATAGACATTG ACATGGAAAA GAGATTTAAT GTTTTGAAAA 900
AAAAACTTTA TATTAACCTG GTAACATCCT CCTGATGAGA AGTACTATAT TAAATATAAA 960
CCCATTATGT TATAAAAAAA AAAA                                     984

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(2) INFORMATION FOR SEQ ID NO:174:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 59 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

```

Met Thr Ser Val Ser Thr Gln Leu Ser Leu Val Leu Met Ser Leu Leu
  1                      5                      10                     15

Leu Val Leu Pro Val Val Glu Ala Val Glu Ala Gly Asp Ala Ile Ala
                20                      25                     30

Leu Leu Leu Gly Val Val Leu Ser Ile Thr Gly Ile Cys Ala Cys Leu
                35                      40                     45

Gly Val Tyr Ala Arg Lys Arg Asn Gly Gln Met
  50                      55

```

(2) INFORMATION FOR SEQ ID NO:175:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

GTTCTTACAG CGGTGAGAGT GAAATGTG

28

(2) INFORMATION FOR SEQ ID NO:176:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

CCGATACACC AAAGTCTCAT CCCTAAAT

28

(2) INFORMATION FOR SEQ ID NO:177:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

GAGTAGTGT GAAGACAAT AAGCAGAA

28

(2) INFORMATION FOR SEQ ID NO:178:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

GTCGCTAACA TCAGAACTAA CAGATTCA

28

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

GAGATACTGC AAATGAATTT ACACGGGT

28

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

GTCACACTTA ACTCCCATCA CCCGAAAG

28

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

TCTGAGGCAC TGATCCTTCT GGCAGTTG

28

(2) INFORMATION FOR SEQ ID NO:182:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 28 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid  
 (A) DESCRIPTION: /desc = "oligonucleotide"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

TGAGGGCTGA AGGTTCCAAA GAAATGGT

28

(2) INFORMATION FOR SEQ ID NO:183:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1528 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid  
 (A) DESCRIPTION: /desc = "oligonucleotide"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

CGCTTTTTTT TTTTTTTTGA CAAGATGGCG GCAGGAGGCA GTGGCGTTGG TGGGAAGCGC 60  
 AGCTCGAAAA GCGATGCCGA TTCTGTTTTC CTGGGCGTGC GCCCACCTTC GGTGACCCA 120  
 GCGCTGAGGC GCGCGCGCGG AGGCCCAAGA AATAAAGAAG GGGGCTGGCG GCGGCTTGCT 180  
 CAGGAGCCGC TGGGGCTGGA GGTGACCAG TTCTGGAAG ACGTGCGGCT ACAGGAGCGC 240  
 ACGAGCGGTG GCTTGTGTTC AGAGGCCCCA AATGAAAAAC TCTTCTTCGT GGACACTGGC 300  
 TCCAAGGAAA AAGGGCTGAC AAAGAAGAGA ACCAAAGTCC AGAAGAAGCT ACTGCTTCTC 360  
 AAGAAACCCC TTCCGGTTGA CCTCATCTCT GAGAACACAT CCAAAGTCCC TGCCCCCAAA 420  
 GACGTCCTCG CCCACAGGT CCCCAACGCC AAGAAGCTCA GCGGAAGGA GCAGCTATGG 480  
 GAGAAGCTGG CCAAGCAGGG CGAGCTGCCC CGGAGGTGTC GCAGGGCCCA GCCCCGGCTC 540  
 CTCACCCCTT CTGCAACAAG GGCCAAGCCC GGGCCCCAGG ACACCGTAGA GCGGCCCTTC 600  
 TACGACCTCT GGGCCTCAGA CAACCCCTG GACAGCCGCT TGGTTGGCCA GGATGAGTTT 660  
 TTCTGGAGC AGACCAAGAA GAAAGGAGTG AAGCGCCGAG CACGCTGCA CACCAAGCCG 720  
 TCCGAGGCGC CGGCCGTGGA GGTGGCGCCT GCCGGAGCTT CTACAATCC ATCCTTTGAA 780  
 GACCACCAGA CCCTGTCTCT AGCGGCCAC GAGGTGGAGT TGCAGCGGCA GAAGGAGCGC 840  
 GAGAAGCTGG AGCGGCAGCT GGCCTTGCCC GCCATGGAGC AGGCCGCCAC CCAGGAGTCC 900  
 ACATTCCAGG AGCTGTGCGA GGGGCTGCTG GAGGAGTCGG ATGGTAGGGG GGAGCCAGGC 960  
 CAGGGCGAGG GGCAGGAGCG TGGGGATGCC GAGGTCTGTC CCACGCCGCG CCGCTTGCC 1020  
 ACCACAGAGA AAGAAGACGA GCAGCAGCGG CGCGCGGAGA AGGCTGTGCA CAGGCTGCGG 1080  
 GTACAGAGCG CCGCGTTGCG GGCAGCCCGG CTCGCGCACC AGGAGCTGTT CCGGCTGCGC 1140  
 GGGATCAAGG CCCAGGTGCG CCTGAGGCTG CGCGAGCTGG CGCGCGCGCG GAGGCGCGCG 1200  
 CAGGCGCGCG GGAAGGCTGA GGCTGACAAG CCCCAGAGGC TGGGACGGCT CAAGTACCAG 1260  
 GCACCTGACA TCGACCTGCA GCTGAGCTCG GAGCTGACAG ACTCGCTCAG GACCCCTGAA 1320  
 CCCGAGGCA ACATCTCTCG AGACCGGTTT AAGAGCTTCC AGAGGAGGAA TATGATGAG 1380  
 CCTCGAGAGA GAGCCAAGT CAAACGCAAG TACAAGTGA AGCTGGTGA GAAGCGGCGC 1440  
 TTCCGTGAGA TCCAGTTGTA GCTGCCATGA GATGCCGAG ACTCGCCCTT CAATAAAAAA 1500  
 TCTCTTCTAG CTGAAAAAAA AAAAAAAA 1528



(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

Met Ala Ala Gly Gly Ser Gly Val Gly Gly Lys Arg Ser Ser Lys Ser  
1 5 10 15  
Asp Ala Asp Ser Gly Phe Leu Gly Leu Arg Pro Thr Ser Val Asp Pro  
20 25 30  
Ala Leu Arg Arg Arg Arg Arg Gly Pro Arg Asn Lys Lys Arg Gly Trp  
35 40 45  
Arg Arg Leu Ala Gln Glu Pro Leu Gly Leu Glu Val Asp Gln Phe Leu  
50 55 60  
Glu Asp Val Arg Leu Gln Glu Arg Thr Ser Gly Gly Leu Leu Ser Glu  
65 70 75 80  
Ala Pro Asn Glu Lys Leu Phe Phe Val Asp Thr Gly Ser Lys Glu Lys  
85 90 95  
Gly Leu Thr Lys Lys Arg Thr Lys Val Gln Lys Lys Ser Leu Leu Leu  
100 105 110  
Lys Lys Pro Leu Arg Val Asp Leu Ile Leu Glu Asn Thr Ser Lys Val  
115 120 125  
Pro Ala Pro Lys Asp Val Leu Ala His Gln Val Pro Asn Ala Lys Lys  
130 135 140  
Leu Arg Arg Lys Glu Gln Leu Trp Glu Lys Leu Ala Lys Gln Gly Glu  
145 150 155 160  
Leu Pro Arg Glu Val Arg Arg Ala Gln Ala Arg Leu Leu Asn Pro Ser  
165 170 175  
Ala Thr Arg Ala Lys Pro Gly Pro Gln Asp Thr Val Glu Arg Pro Phe  
180 185 190  
Tyr Asp Leu Trp Ala Ser Asp Asn Pro Leu Asp Arg Pro Leu Val Gly  
195 200 205  
Gln Asp Glu Phe Phe Leu Glu Gln Thr Lys Lys Lys Gly Val Lys Arg  
210 215 220  
Pro Ala Arg Leu His Thr Lys Pro Ser Gln Ala Pro Ala Val Glu Val  
225 230 235 240

Ala Pro Ala Gly Ala Ser Tyr Asn Pro Ser Phe Glu Asp His Gln Thr  
245 250 255

Leu Leu Ser Ala Ala His Glu Val Glu Leu Gln Arg Gln Lys Glu Ala  
260 265 270

Glu Lys Leu Glu Arg Gln Leu Ala Leu Pro Ala Met Glu Gln Ala Ala  
275 280 285

Thr Gln Glu Ser Thr Phe Gln Glu Leu Cys Glu Gly Leu Leu Glu Glu  
290 295 300

Ser Asp Gly Glu Gly Glu Pro Gly Gln Gly Glu Gly Pro Glu Ala Gly  
305 310 315 320

Asp Ala Glu Val Cys Pro Thr Pro Ala Arg Leu Ala Thr Thr Glu Lys  
325 330 335

Lys Thr Glu Gln Gln Arg Arg Arg Glu Lys Ala Val His Arg Leu Arg  
340 345 350

Val Gln Gln Ala Ala Leu Arg Ala Ala Arg Leu Arg His Gln Glu Leu  
355 360 365

Phe Arg Leu Arg Gly Ile Lys Ala Gln Val Ala Leu Arg Leu Ala Glu  
370 375 380

Leu Ala Arg Arg Arg Arg Arg Gln Ala Arg Arg Glu Ala Glu Ala  
385 390 395 400

Asp Lys Pro Arg Arg Leu Gly Arg Leu Lys Tyr Gln Ala Pro Asp Ile  
405 410 415

Asp Val Gln Leu Ser Ser Glu Leu Thr Asp Ser Leu Arg Thr Leu Lys  
420 425 430

Pro Glu Gly Asn Ile Leu Arg Asp Arg Phe Lys Ser Phe Gln Arg Arg  
435 440 445

Asn Met Ile Glu Pro Arg Glu Arg Ala Lys Phe Lys Arg Lys Tyr Lys  
450 455 460

Val Lys Leu Val Glu Lys Arg Ala Phe Arg Glu Ile Gln Leu  
465 470 475

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

```

ACAAGATGGC GGCGCCGAAG GGGAGCCTCT GGGTGAGGAC CCAACTGGGG CTCCC GCCGC 60
TGCTGCTGCT GACCATGGCC TTGGCCCGAG GTTCGGGGAC CGCTTCGGCT GAAGCATTGG 120
ACTCGGTCTT GGGTGATACG GCGTCTTGCC ACCGGGCCCTG TCAGTTGACC TACCCCTTGC 180
ACACCTACCC TAAGGAAGAG GAGTGTGACG CATGTCAGAG AGGTTGCAGG CTGTTTTCAA 240
TTTGTCAGTT TGTGGATGAT GGAATTGACT TAAATCGAAC TAAATTGGAA TGTGAATCTG 300
CATGTACAGA AGCATATTCC CAATCTGATG AGCAATATGC TTGCCATCTT GGTGTCAGA 360
ATCAGCTGCC ATTTCGCTGAA CTGAGACAAG AACAACTTAT GTCCCTGATG CCAAAAATGC 420
ACCTACTCTT TCCTCTAACT CTGGTGAGGT CATTCCTGGG TGACATGATG GACTCCGCAC 480
AGAGCTTCAT AACCTCTTCA TGGACTTTTT ATCTTCAAGC CGATGACCGA AAAATAGTTA 540
TATTCCAGTG TAAGCCAGAA ATCCAGTACG CACCACATTT GGAGCAGGAG CCTACAAATT 600
TGAGAGAATC ATCTCTAAGC AAAATGTCTT CAGATCTGCA AATGAGAAAT TCACAGAGCG 660
ACAGGAATTT TCTTGAAGAT GGAGAAAGTG ATGGCTTTTT AAGATGCCTC TCTCTTAACT 720
CTGGGTGGAT TTTAACTACA ACTCTTGTCC TCTCGGTGAT GGTATTGCTT TGGATTGTGT 780
GTGCAACTGT TGCTACAGCT GTGGAGCAGT ATGTTCCCTC TGAGAAGCTG AGTATCTATG 840
GTGACTTGGA GTTTATGAAT GAACAAAAGC TAAACAGATA TCCAGCTTCT TCTCTTGTGG 900
TTGTTAGATC TAAAACTGAA GATCATGAAG AAGCAGGGCC TCTACCTACA AAAGTGAATC 960
TTGCTCATTC TGAATTTTAA GCATTTTTCT TTTAAAGAC AAGTGTATA GACATCTAAA 1020
ATTCACATCC TCAATAGAGT TTTAAATGG TTTTATTGGA TATAGCCCTT AAGAAATCAC 1080
TATAAAATGT AAATAAAGTT ACTCAAATCT GTGAAGACTG TATTTGCTAT AACTTTATTG 1140
GTATTGTTTT TGTAGTAATT TAAGAGGTGG ATGTTTGGGA TTGTATTATT ATTTTACTAA 1200
TATCTGTAGC TATTTTGTGT TTTGCTTTGG TTATTGTTTT TTTCCCTTTT CTTAGCTATG 1260
AGCTGATCAT TGCTCCTTCT CACCTCCTGC CATGATACG TCAGTTACCT TAGTTAACAA 1320
GCTGAATATT TAGTAGAAAT GATGCTTCTG CTCAGGAATG GCCCACAAAT CTGTAATTGT 1380
AAATTTAGCA GGAATATGACC TTTAATGACA CTACATTTTC AGGAACTGAA ATCATTAAAA 1440
TTTTATTGTA ATAATTAATA AAAAAAAAAA AA 1472

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(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

```

Met Ala Ala Pro Lys Gly Ser Leu Trp Val Arg Thr Gln Leu Gly Leu
 1             5             10             15

Pro Pro Leu Leu Leu Leu Thr Met Ala Leu Ala Gly Gly Ser Gly Thr
 20             25             30

Ala Ser Ala Glu Ala Phe Asp Ser Val Leu Gly Asp Thr Ala Ser Cys
 35             40             45

His Arg Ala Cys Gln Leu Thr Tyr Pro Leu His Thr Tyr Pro Lys Glu
 50             55             60

Glu Glu Leu Tyr Ala Cys Gln Arg Gly Cys Arg Leu Phe Ser Ile Cys
 65             70             75             80

Gln Phe Val Asp Asp Gly Ile Asp Leu Asn Arg Thr Lys Leu Glu Cys
 85             90             95

```

Glu Ser Ala Cys Thr Glu Ala Tyr Ser Gln Ser Asp Glu Gln Tyr Ala  
 100 105 110  
 Cys His Leu Gly Cys Gln Asn Gln Leu Pro Phe Ala Glu Leu Arg Gln  
 115 120 125  
 Glu Gln Leu Met Ser Leu Met Pro Lys Met His Leu Leu Phe Pro Leu  
 130 135 140  
 Thr Leu Val Arg Ser Phe Trp Ser Asp Met Met Asp Ser Ala Gln Ser  
 145 150 155 160  
 Phe Ile Thr Ser Ser Trp Thr Phe Tyr Leu Gln Ala Asp Asp Gly Lys  
 165 170 175  
 Ile Val Ile Phe Gln Ser Lys Pro Glu Ile Gln Tyr Ala Pro His Leu  
 180 185 190  
 Glu Gln Glu Pro Thr Asn Leu Arg Glu Ser Ser Leu Ser Lys Met Ser  
 195 200 205  
 Ser Asp Leu Gln Met Arg Asn Ser Gln Ala His Arg Asn Phe Leu Glu  
 210 215 220  
 Asp Gly Glu Ser Asp Gly Phe Leu Arg Cys Leu Ser Leu Asn Ser Gly  
 225 230 235 240  
 Trp Ile Leu Thr Thr Thr Leu Val Leu Ser Val Met Val Leu Leu Trp  
 245 250 255  
 Ile Cys Cys Ala Thr Val Ala Thr Ala Val Glu Gln Tyr Val Pro Ser  
 260 265 270  
 Glu Lys Leu Ser Ile Tyr Gly Asp Leu Glu Phe Met Asn Glu Gln Lys  
 275 280 285  
 Leu Asn Arg Tyr Pro Ala Ser Ser Leu Val Val Val Arg Ser Lys Thr  
 290 295 300  
 Glu Asp His Glu Glu Ala Gly Pro Leu Pro Thr Lys Val Asn Leu Ala  
 305 310 315 320  
 His Ser Glu Ile

(2) INFORMATION FOR SEQ ID NO:187:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1573 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

GTGATTGGTA CAGTAGGTTT ATAAACAGAA GTTTAAACTT GTAAGCTTAA GCTTCCGTTT  
 ATAAACAGAA GTTTAAAAAT ATAGGTCCTG TTAAACATTC AGCTCTGTTA ACTCACTCAT

60  
 120

CTTTTGTGT TTTTACACTT TGTCAAGATT TCTTTACATA TTCATCAATG TCTGAAGAAG 180  
TACTTATTGC AGACTCTCAA TTCCAGAACT CCAGTGAGAT GGAAAAAATC CCAGAAATTG 240  
GCAAAATTTGG GGAAAAAGCA CCTCCAGCTC CCTCTCATGT ATGGCGTCCA GCAGCCTTGT 300  
TTCTGACTCT TCTGTGCCTT CTGTTGCTCA TTGGATTGGG AGCTCTGGCA AGCATGTTC 360  
ATGTAACCTT GAAGATAGAA ATGAAAAAAA TGAACAAACT ACAAACATC AGTGAAGAGC 420  
TCCAGAGAAA TATTTCTCTA CAATGATGA GTAACATGAA TATCTCCAAC AAGATCAGGA 480  
ACCTCTCCAC CACACTGCAA ACAATAGCCA CCAAAATTATG TCGTGAGCTA TATAGCAAG 540  
AACAAAGACA CAAATGTAAG CCTTGTCCAA GGAGATGGAT TTGCGATAAG GACAGCTGTT 600  
ATTTCTTAAG TGATGATGTC CAAACATGGC AGGAGAGTAA AATGGCCTGT GCTGCTCAGA 660  
ATGCCAGCCT GTTGAAGATA AACCAACAAA ATGCATTGGA ATTTATAAAA TCCCAGAGTA 720  
GATCATATGA CTATTGGCTG GGATTATCTC CTGAAGAAGA TTCCACTCGT GGTATGAGAG 780  
TGGATAATAT AATCCACTCC TCTGCCTGGG TTATAAGAAA CGCACTCTGA TTAATAACA 840  
TGTATTGTGG ATATATAAAT AGACTATATG TTCAATATTA TCACTGCACT TATAAACAAA 900  
GAATGATATG TGAGAAGATG GCCAATCCAG TGCAGCTTGG TTCTACATAT TTTAGGGAGG 960  
CATGAGGCAT CAATCAAATA CATTGAAGGA GTGTAGGGGG TGGGGTCTT AGGCTATAGG 1020  
TAAATTTAAA TATTTTCTGG TTGACAATTA GTTGAGTTTG TCTGAAGACC TGGGATTTTA 1080  
TCATGCAGAT GAAACATCCA GGTAGCAAGC TTCAGAGAGA ATAGACTGTG AATGTTAATG 1140  
CCAGAGAGGT ATAATGAAGC ATGTCCMACY TCCCACTTTC CATCATGGCY TGAACCCYKG 1200  
RGAAGAGGA AGTCCATTCA GATAGTTGTG GGGGGCCTTS GAATTTTCAT TTTCAWWAC 1260  
GTTCTTCCCC TTCTGGCCAA GATTGGCCAG AGGCAACATC AAAAACCAGC AATTKTAT 1320  
TTTGTCACC ACAGSCTTCTA GGGTGGCATG GYTCCCATC TSGGGTCCAT CCTAWACTTC 1380  
CATGGGACCT CCTATGGCTG AAGGCCTTAT GAGTCAAAGG ACTTATAGCC AATTGATTGT 1440  
TTTAGGCCAG GTAAGAATGG ATATGGACAT GCATTATTA CYTYTTAAAA TTATTATTTT 1500  
AAGTAAAGC AATAAACAA AANGNAAAG GCAAAAAAAA AAAAAAAA AAAAAAAA 1560  
AAAAAAA AAA 1573

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

Met Ser Glu Glu Val Thr Tyr Ala Asp Leu Gln Phe Gln Asn Ser Ser  
1 5 10 15  
Glu Met Glu Lys Ile Pro Glu Ile Gly Lys Phe Gly Glu Lys Ala Pro  
20 25 30  
Pro Ala Pro Ser His Val Trp Arg Pro Ala Ala Leu Phe Leu Thr Leu  
35 40 45  
Leu Cys Leu Leu Leu Ile Gly Leu Gly Val Leu Ala Ser Met Phe  
50 55 60  
His Val Thr Leu Lys Ile Glu Met Lys Lys Met Asn Lys Leu Gln Asn  
65 70 75 80  
Ile Ser Glu Glu Leu Gln Arg Asn Ile Ser Leu Gln Leu Met Ser Asn  
85 90 95  
Met Asn Ile Ser Asn Lys Ile Arg Asn Leu Ser Thr Thr Leu Gln Thr  
100 105 110  
Ile Ala Thr Lys Leu Cys Arg Glu Leu Tyr Ser Lys Glu Gln Glu His  
115 120 125  
Lys Cys Lys Pro Cys Pro Arg Arg Trp Ile Trp His Lys Asp Ser Cys  
130 135 140  
Tyr Phe Leu Ser Asp Asp Val Gln Thr Trp Gln Glu Ser Lys Met Ala  
145 150 155 160

Cys	Ala	Ala	Gln	Asn	Ala	Ser	Leu	Leu	Lys	Ile	Asn	Asn	Lys	Asn	Ala
				165					170					175	
Leu	Glu	Phe	Ile	Lys	Ser	Gln	Ser	Arg	Ser	Tyr	Asp	Tyr	Trp	Leu	Gly
			180					185					190		
Leu	Ser	Pro	Glu	Glu	Asp	Ser	Thr	Arg	Gly	Met	Arg	Val	Asp	Asn	Ile
			195				200					205			
Ile	His	Ser	Ser	Ala	Trp	Val	Ile	Arg	Asn	Ala	Pro	Asp	Leu	Asn	Asn
			210			215					220				
Met	Tyr	Cys	Gly	Tyr	Ile	Asn	Arg	Leu	Tyr	Val	Gln	Tyr	Tyr	His	Cys
					230					235					240
Thr	Tyr	Lys	Gln	Arg	Met	Ile	Cys	Glu	Lys	Met	Ala	Asn	Pro	Val	Gln
				245					250					255	
Leu	Gly	Ser	Thr	Tyr	Phe	Arg	Glu	Ala							
			260					265							

(2) INFORMATION FOR SEQ ID NO:189:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 618 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

GAGTTATATG	ACACTCAAAG	GAAAAGCAAA	AGAGCATTAA	GAAGTGTCTG	TTTTTGTAT	60
TGCCATTTC	TAAATATTTT	AGTAGGTGTT	CAATTTCATT	GGATATTCCT	TTTTTTTAA	120
TGCTCTTTGA	CCTATGATTG	AAAACAGTAG	TGGTCTATG	ACTTTTGAGG	AGAGGGAGAA	180
CCGAAGATTA	CAGGAGGCCA	GCATGAGGTT	GGAACAAGAG	AATGATGACC	TTGCCCATGA	240
ACTAGTAACA	AGCAAAATTG	CTCTACGGAA	TGACTTGGAT	CAGGCAGAAG	ACAAGGCAGA	300
TGTGTTGAAT	AAAGAGCTCC	TTTTTGACAA	ACAGAGGCTG	GTGGAGACTG	AAGAGGAGAA	360
GAGGAAGCAA	GAGGAAGAGA	CTGCCCAGCT	AAAAGAAGTC	TTCAGGAAC	AGCTAGAGAA	420
GCGAATAT	GAATAAAGA	AGACTACAGC	TATCATTGCT	GAGTATAAAC	AGGTAATGTA	480
CTTCTGTGGC	ACATAGAGCT	AGTTATAGTT	TGCTGCTATA	AAAGTAATTT	TTTTTTTTTT	540
TGCTTGAGG	CCAGGAGTTT	GAGACTAGCC	TGAGCAACAT	AGCAGGACTC	CGTCCCAAGG	600
AAAAAAAAAA	AAAAAAAAAA					618

(2) INFORMATION FOR SEQ ID NO:190:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 120 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

Met	Ile	Glu	Asn	Ser	Ser	Trp	Ser	Met	Thr	Phe	Glu	Glu	Arg	Glu	Asn
1			5					10					15		
Arg	Arg	Leu	Gln	Glu	Ala	Ser	Met	Arg	Leu	Glu	Gln	Glu	Asn	Asp	Asp
			20					25					30		
Leu	Ala	His	Glu	Leu	Val	Thr	Ser	Lys	Ile	Ala	Leu	Arg	Asn	Asp	Leu
			35				40					45			
Asp	Gln	Ala	Glu	Asp	Lys	Ala	Asp	Val	Leu	Asn	Lys	Glu	Leu	Leu	Leu
			50			55				60					
Thr	Lys	Gln	Arg	Leu	Val	Glu	Thr	Glu	Glu	Glu	Lys	Arg	Lys	Gln	Glu
			65			70				75				80	
Glu	Glu	Thr	Ala	Gln	Leu	Lys	Glu	Val	Phe	Arg	Lys	Gln	Leu	Glu	Lys
				85				90						95	

Ala Glu Tyr Glu Ile Lys Lys Thr Thr Ala Ile Ile Ala Glu Tyr Lys  
 100 105 110  
 Gln Val Met Tyr Phe Cys Gly Thr  
 115 120

(2) INFORMATION FOR SEQ ID NO:191:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 510 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: cDNA  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

TGCAGAAATCC AGAATGGATG TCCTCTTTGT AGCCATCTTT GCTGTGCCAC TTATCTGGG 60  
 ACAAGAATAT GAGGATGAAG AAAGACTGGG AGAGGATGAA TATTATCAGG TGGTCTATTA 120  
 TTATACAGTC ACCCCCACTT ATGATGACTT TAGTGCAGAT TTCACCATG ATTACTCCAT 180  
 ATTTGAGTCA GAGGACAGGC TGAACAGGTT GGATAAGGAC ATAACAGAAG CAATAGAGAC 240  
 TACCATTAGT CTTGAAACAG CACGTGCAGA CCATCCGAAG CCTGTAAGT TGAAACCACT 300  
 AACAAACGGAA CCTAGTCCAG ATCTGAACGA TGCCGTGTCC AGTTTGCGAA GTCCTATTCC 360  
 CCTCCTCCTG TCGTGTGCCT TTGTTCCAGT GGGGATGTAT TTCATGTAGA AGGTGGAAGA 420  
 AGGCTGCTAT GACTCTTTGG ATGGGAGTCT GGCAAGAGGA AATTGGAAGA TAAATAAAT 480  
 AATAAGTGAA ATAAAAAAA AAAAAAAA 510

(2) INFORMATION FOR SEQ ID NO:192:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 131 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

Met Asp Val Leu Phe Val Ala Ile Phe Ala Val Pro Leu Ile Leu Gly  
 1 5 10 15  
 Gln Glu Tyr Glu Asp Glu Glu Arg Leu Gly Glu Asp Glu Tyr Tyr Gln  
 20 25 30  
 Val Val Tyr Tyr Thr Val Thr Pro Ser Tyr Asp Asp Phe Ser Ala  
 35 40 45  
 Asp Phe Thr Ile Asp Tyr Ser Ile Phe Glu Ser Glu Asp Arg Leu Asn  
 50 55 60  
 Arg Leu Asp Lys Asp Ile Thr Glu Ala Ile Glu Thr Thr Ile Ser Leu  
 65 70 75 80  
 Glu Thr Ala Arg Ala Asp His Pro Lys Pro Val Thr Val Lys Pro Val  
 85 90 95  
 Thr Thr Glu Pro Ser Pro Asp Leu Asn Asp Ala Val Ser Ser Leu Arg  
 100 105 110  
 Ser Pro Ile Pro Leu Leu Leu Ser Cys Ala Phe Val Gln Val Gly Met  
 115 120 125  
 Tyr Phe Met  
 130

(2) INFORMATION FOR SEQ ID NO:193:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 883 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

```

CATCTGACCA TCCATATCCA ATGTTCTCAT TTAACATTA CCCAGCATCA TTGTTTATAA      60
TCAGAAACTC TGGTCCTTCT GTCTGGTGGC ACTTAGAGTC TTTTGTGCCA TAATGCAGCA      120
GTATGGAGGG AGGATTTTAT GGAGAAATGG GGATAGTCTT CATGACCACA AATAAATAAA      180
GGAAACTATA GCTGCATTGT GGGTTTTGAA AAGGTTATTA TACTTCTTAA CAATCTCTTT      240
TTTCAGGGAC TTTTCTAGCT GTATGACTGT TACTTGACCT TCTTTGAAAA GCATTCCTCAA      300
AATGCTCTAT TTTAGATAGA TTAACATTAA CCAACATAAT TTTTTTTAGA TCGAGTCAGC      360
ATAAATTTCT AAGTCAGCCT CTAGTCGTGG TTCATCTCTT TCACCTGCAT TTTATTTGGT      420
GTTTGTCTGA AGAAAGGAAA GAGGAAAGCA AATACGAATT GTACTATTGT TACCAATCTC      480
TTGGGATTCA TTGGCAATAA ATTTCAAGTG GGTGTATTAT TAAATAGAAA AAAAAAATTT      540
TGTTTCCCTAG GTTGAAGGTC TAATTGATAC GTTTGACTTA TGATGACCAT TTATGCACTT      600
TCAAAATGAAT TTGCTTTCAA AATAAATGAA GAGCAGCTGT CCTTCTTTCC TCTTTTAAAGT      660
GTTCAAGCTGT GGCATGCTCA GAGGTTCCTG CTGGATTCCA GCTGGAGCGG TGTGATACCC      720
TTCCTTTTCA GCTGTTCCGT CCTTCTTTTC TTGTATCCAC CAAAGTGGAG ACAAAATACAT      780
GATCTCAAAG ATACACAGTA CCTACTTAAT TCCAGCTGAT GGGAGACCAA AGAATTTGCA      840
AGTGATGGT TTGATATCAC TGTAAATAAA AAGAGGGCCT GGG                          883

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- (2) INFORMATION FOR SEQ ID NO:194:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 79 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: protein  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

```

Met Met Thr Ile Tyr Ala Leu Ser Asn Glu Phe Ala Phe Lys Ile Asn
1          5          10          15
Glu Glu Gln Leu Ser Phe Phe Pro Leu Leu Ser Val Gln Leu Trp His
20          25          30
Ala Gln Arg Phe Leu Leu Asp Ser Ser Trp Ser Gly Val Ile Pro Phe
35          40          45
Phe Phe Ser Cys Ser Cys Leu Pro Phe Leu Tyr Pro Pro Lys Trp Arg
50          55          60
Gln Ile His Asp Leu Lys Asp Thr Gln Tyr Leu Leu Asn Ser Ser
65          70          75

```

- (2) INFORMATION FOR SEQ ID NO:195:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 110 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

```

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA      60
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA      110

```

- (2) INFORMATION FOR SEQ ID NO:196:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 861 base pairs



- (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: cDNA  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

```

TAGGCGCTCTT TGGCCGGTGC TGCCCTGAGAA GGATTGGCAC GGGCACAGAC CACTGCCCCC      60
ACCTGCCCGCTG CGCCATCTAC CCAAGAAGGC TCGGCACGGG CACCAACCAC TGCCCTCCAAC      120
TGCCCCCATGCT TGCCCTGAGAA GGCACCTGCAC GGCCACCCCC AACTGCCCGG CACTGTCCCT      180
ACCCGGGCGAG CCATGCGGAGC GGCTGGAACT CTGCTGGCCT TCTGCTGCCT GGTCTTGAGC      240
ACCACTTGGGG GCCCTTCCCC AGATACTTGT TCCCAGGACC TTAACCTCACG TGTGAAGCCA      300
GGATTTCCTTA AAACAATAAA GACCAATGAC CCAGGAGTCC TCCAAGCAGC CAGATACAGT      360
GTTGAAAGAT TCAACAACCTG CACGAACGAC ATGTTCTTGT TCAAGGAGTC CCGCATCACA      420
AGGGGCCCTTAG TTCAGATAGT GAAAGGCCTG AATATATATGC TCGARGTGGA AATTGGCAGA      480
ACTACCTGCA AGAAAAACCA GCACCTGCGT CTGGATGACT GTGACTTCCA AACCAACCAC      540
ACCTTGAAAGC AGACTCTGAG CTGCTACTCT GAAGTCTGGG TCGTGCCCTG GCTCCAGCAC      600
TTCGAGGTGC CTGTTCTCCG TTGTCACTGA CCCCCGCTC TTCAGCAAGA CCACAGCCAT      660
GACAAACACC AGGATGCTATG CTCTCTTGTC CCTCCACCC GCYWSRTGAC CCRRCCTTAC      720
AGACCCTCTC RGGCCTCWGA CGAGTGAGCG GRTGAAGTGC MAYTGGGTTSA CMGCGAGGCA      780
GCTRGAATGG CAGCWTGGTA GCGCCTCCTA ACAGRTTAAA TRGATCACAT GTGMTTCTAA      840
AATTAAAAAA AAAAAAAAAA A

```

- (2) INFORMATION FOR SEQ ID NO:197:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 167 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

```

Met Leu Pro Glu Lys Ala Leu His Gly His Pro Gln Leu Pro Arg Thr
1          5          10          15
Val Pro Thr Arg Ala Ala Met Arg Ala Ala Gly Thr Leu Leu Ala Phe
20          25          30
Cys Cys Leu Val Leu Ser Thr Thr Gly Gly Pro Ser Pro Asp Thr Cys
35          40          45
Ser Gln Asp Leu Asn Ser Arg Val Lys Pro Gly Phe Pro Lys Thr Ile
50          55          60
Lys Thr Asn Asp Pro Gly Val Leu Gln Ala Ala Arg Tyr Ser Val Glu
65          70          75
Lys Phe Asn Asn Cys Thr Asn Asp Met Phe Leu Phe Lys Glu Ser Arg
85          90          95
Ile Thr Arg Ala Leu Val Gln Ile Val Lys Gly Leu Lys Tyr Met Leu
100         105         110
Glu Val Glu Ile Gly Arg Thr Thr Cys Lys Lys Asn Gln His Leu Arg
115         120         125
Leu Asp Asp Cys Asp Phe Gln Thr Thr Asn His Thr Leu Lys Gln Thr Leu
130         135         140
Ser Cys Tyr Ser Glu Val Trp Val Val Pro Trp Leu Gln His Phe Glu
145         150         155         160
Val Pro Val Leu Arg Cys His
165

```

- (2) INFORMATION FOR SEQ ID NO:198:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: other nucleic acid  
 (A) DESCRIPTION: /desc = "oligonucleotide"  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

ANCCAGAATC GGCATCGCTT TTCGAGCTG 29

(2) INFORMATION FOR SEQ ID NO:199:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 29 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: other nucleic acid  
 (A) DESCRIPTION: /desc = "oligonucleotide"  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

TNTGGTGCGT ACTGGATTTC TGGCTTAGA 29

(2) INFORMATION FOR SEQ ID NO:200:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 29 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: other nucleic acid  
 (A) DESCRIPTION: /desc = "oligonucleotide"  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

GNTAACAGAG CTGAATGTTA AACAGGACC 29

(2) INFORMATION FOR SEQ ID NO:201:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 29 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: other nucleic acid  
 (A) DESCRIPTION: /desc = "oligonucleotide"  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

NTCTCTCAA AGTCATAGAC CAACTACTG 29

(2) INFORMATION FOR SEQ ID NO:202:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 29 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: other nucleic acid  
 (A) DESCRIPTION: /desc = "oligonucleotide"  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

GNTCAGCCTG TCCTCTGACT CAAATATGG 29

- (2) INFORMATION FOR SEQ ID NO:203:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 29 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: other nucleic acid
    - (A) DESCRIPTION: /desc = "oligonucleotide"
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

TNACCTGCAT TTTATTGGT GTTTGTCTG

29

- (2) INFORMATION FOR SEQ ID NO:204:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 29 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: other nucleic acid
    - (A) DESCRIPTION: /desc = "oligonucleotide"
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

TNAACACTGT ATCTGGCTGC TTGGAGGAC

29

- (2) INFORMATION FOR SEQ ID NO:205:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 2556 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

GCAAGATTGG GCCTGGATTC TTCTGAGGAT GTGAAGTAAT GGAAACAGTA AGACTGTTCC	60
AGACTAGGGG AAGACTAGAG ACCTAATAGC TGGATTCCAT GTGATCTTTT GTTGGACTTT	120
GGGATTGGAG GTGAGAGTAG AGAAGGCATA ATGCACGTTT TTGAGACGAG GGAAATGTGA	180
ATATAGCCCTG TATGCTTACA CTCAGTCTG AAGACATGTW AACCATGTCT ATACTAACCA	240
GCCAAATATT TGAACACTAA AAGGAAGAAT TTTCTTAATG TGGTAATGGT WTCATGGTTG	300
TATAGATGTT TCCTCCTCTT GGSAGATGTG TGTGAAAAT AGGGTTTGAC GTCTAAACCT	360
ATTTTGTGTTT GGCAAAAAGG ACGTGTGTCT GTACAAAAGA AGTGGAGCCA GTATGGCAAA	420
ATGTTTACMA GGA CTCTGGG TGAGARGTWC ATAGTGCTT ACTATACTGT TTTGTTCTG	480
AATTTGGAAT TTCTCAAAAT TAAAAAATA TCTACTGAGG AGCTTTTCGT TTTAACTGGT	540
GGGGAATGGG TTCTGGGTGG TTTTGCCCTT TTTCTTTTGA GATTCAAGAA ATCCATGGTG	600

AAAGGTTTGG ATTCTATGA AGAAAAGGAG GATAAAGTGA TCAAGGAGAT GGCAGCTCAG	660
ATCCGTGAGG TGGAGCAGAG CCGACAGGAG GTGGTTCGGT CTGTCTTAGA GGTGTGGTTTC	720
CCTCGGAGGA TCCAGACCAC CTCAGGCAGT GCCAGACCCA GAAGAGGGCT CTCAGCACC	780
TAGAAGCTGG AAAGGGATGA ACAGGTAAGA CTATTAGGGA ATCTCTTGTT GGAATTGTA	840
CATCTTAGAA CATCTGCAA CCTTTTGCTT GGGAAATGGA AACAGATCTA ATCTTTACCA	900
CCCTCATGGC TCAAGGACCT CATCTGGCAG CCTGGCTCAT GTTTTTCAGC CAAGTAGCTT	960
CCAGCTTACA GCAGCCCTCA AATTTGGACC TGCCACCAGC TCCAGAGCTT GACTGGATGG	1020
AGACAGGACC ATCTCTGACA TTCATTGGCC ATCAGGTACA AAGGATAAGC AAGCCAGAAG	1080
AGGGCCAATG GTCCTCAGG TCTCAGGACC CCTTCTCCT GATTTTCTAC CTATTCAAGC	1140
CACTGCTGCC TCCACTGCAG GCTTTTCTCT CTTCCTTAC TGTTCCCTAG TAGTGTCTC	1200
AGACCTCTTC TCACCCTCCA AAGCGATCCT ATTCACATGT ATTGACACTT AGGAGTGCCA	1260
ACTCCTAAAT CTTGCCCTCT GTAGAACTCA TAGTTCCAAC TCAACACAGG ACATTAAATA	1320
TCCCACAGGC ATCTGAAACT AACCCCCACC ACTCCTATAT TTCCAATCAC TAGATGCAGA	1380
TCCTTTCCTT TTCCATCTCC CATATCTGT CAACAAGCGC TCAATTTTAA CCTGTCTGCC	1440
TCCATTACGC CTTTGGGCAA TTTCTACTCC CCCTTCAATC CTGCCTCACA AACAGAAAAT	1500
CATTGTACCA CTTATGATTT TACTCTACAC TTCAGCTGTA TTGTGTGTCT TCGGGCTTTT	1560
GCAGTTGCCA TTGTCTAAAA CATGCTTTCC TTCCCTCATC ACCTAGTTTA CCTTCAACTG	1620
TTAGCTCAAA TGTCACTTT TCATAAAAGG CTTATCTGAA CAGGTTATCT CTATTTCAAG	1680
TGGATGTAGC ACCATGTAAA GTTGCAAATG TAATTACGT AACTTGTGCT TAATGCTCTT	1740
CCCCAATTAT ATGTATGCTG TGAGGGCAAG GTTTTGCTCC CCTGGCATGT AATAGCCACT	1800
CTACTTACAG ACATCTCCAC TGTATGACT GTGAGCTTCC TGAGGACAGG GTTGTCTTAG	1860
AGTGACTTAC TGTGCTTTCA AAGTTTAAAC TCAGCTGGGG TGCAGAATTA GCATTGTGGC	1920
AGCAGTCACA CCCACCTCTT TTAAGTGTG CTTTGTCTAT CGTTTCTAGG ATTTTTTTTT	1980
TTAATCATGC CTAGACTTTA ACTAGCACTT TTTTCCCAT TTCCAACAC AGGATATACC	2040
AGGAGTTGGT AACATCCACT CAGGTGCCAC ACCTCCCTGG ATGATCCAAG ATGAAGAATA	2100
CATTGTGGG AACCAAGAAA TAGGACCATC CTATGAAGAA TTTCTTAAAG AAAAGGAAAA	2160
ACAGAAGTTG AAAAACTCC CCCAGACCG AGTTGGGGCC AACTTTGATC ACAGCTCCAG	2220
GACCAGTGCA GGCTGGCTGC CCTCTTTTGG CCGTGTCTGG AATAATGGAC GCCGCTGGCA	2280

GTCCAGACAT CAATTCAAAA CTGAAGCTGC AGCAATGAAG AAGCAGTCAC ATACAGAAAA 2340  
AAGCTAATCA TGCTCTCTAC CAACTACCAT GAGGCTAAAA GCAAAGTCAA CAAACCCCTA 2400  
TTATACCTTC CACCAAATTC TTTATCATTG TCTTTCTTAG GAAACAGACA TACTCATTCA 2460  
TTTGATTIAA TAAAGTTTTA TTTTTCCTAA GTTACAGCTG GTTGACCTG TAAAAAATAA 2520  
TAAAAGAAT CAGAACCATA AAAAAAAAAA AAAAAA 2556

(2) INFORMATION FOR SEQ ID NO:206:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 104 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

Met Glu Thr Asp Leu Ile Phe Thr Thr Leu Met Ala Gln Gly Pro His  
1 5 10 15  
Leu Ala Ala Trp Leu Met Phe Phe Ser Gln Val Ala Ser Ser Leu Gln  
20 25 30  
Gln Pro Ser Asn Leu Asp Leu Pro Pro Ala Pro Glu Leu Asp Trp Met  
35 40 45  
Glu Thr Gly Pro Ser Leu Thr Phe Ile Gly His Gln Val Gln Arg Ile  
50 55 60  
Ser Lys Pro Glu Glu Gly Gln Trp Ser Leu Arg Ser Gln Asp Pro Phe  
65 70 75 80  
Leu Leu Ile Phe Tyr Leu Phe Lys Pro Leu Leu Pro Pro Leu Gln Ala  
85 90 95  
Phe Pro Ser Ser Phe Thr Val Pro  
100

(2) INFORMATION FOR SEQ ID NO:207:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1276 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

TTCATCTTCT CCCTGTAAC T GAGATTCTA CCACACCTTT GAACAATGTT CTTTCCTTTC	60
TGGTTATCTG AAGACTGTCC TGAAGGAAG ACATAAGTGT TGTGATTAGT AGAAGCTTTC	120
TAGTAGACCA TATTTCTTCT GGATTGTAAT AAAATTGTTA GTAGCTCCTT TTACTTTGTT	180
CCTGTCTCTG GAAAGCCATT TTTGAATTGC TGATTACTTT GGCTTTAATC AGTGGTCACC	240
TAGAAAAAGC TTTGTAATCA TAACACAATG AGTAATCTTT GATAAAAGTT CAGATACAAA	300
AGGAGCACTG TAAAACTGGT AGGAGCTATG GTTTAAGAGC ATTGGAAGTA GTTACAACCTC	360
AAGGATTTTG GTAGAAAGGT ATGAGTTTGG TCGAAAAAAT AAAATAGTGG CAAAATAAGA	420
TTTAGTTGTG TTTTCTCAGA GCCGCCACAA GATTGAACAA AATGTTTTCT GTTTGGGCAT	480
CCTGAGGAAG TTGTATTAGC TGTTAATGCT CTGTGAGTTT AGAAAAAGTC TTGATAGTAA	540
ATCTAGTTTT TGACACAGTG CATGAACATA GTAGTTAAAT ATTTACATAT TCAGAAAGGA	600
ATAGTGGAAG AGGTATCTTG GTTATGACAA AGTCATTACA AATGTGACTA AGTCATTACA	660
AATGTGACTG AGTCATTACA GTGGACCCTC TGGGTGCATT GAAAAGAATC CGTTTTATAT	720
CCAGGTTTCA GAGGACCTGG AATAATAATA AGCTTTGGAT TTTGCATTCA GTGTAGTTGG	780
ATTTTGGGAC CTGCGCTCA GTGTTATTTA CTGGGATTGG CATACGTGTT CACAGGCAGA	840
GTAGTTGATC TCACACAACG GGTGATCTCA CAAACTGGT AAGTTTCTTA TGCTCATGAG	900
CCCTCCCTTT TTTTTTTTAA TTTGGTGCCT GCAACTTTCT TAACAATGAT TCTACTTCCT	960
GGGCTATCAC ATTATAATGC TCTTGGCCTC TTTTGTGCTG CTGTTTGTCT ATTCTTAAAC	1020
TTAGGCCAAG TACCAATGTT GGCTGTTAGA AGGGATTCTG TTCATTCAAC ATGCAACTTT	1080
AGGGAATGGA AGTAAGTTCA TTTTAAAGTT GTGTTGTCAG TAGTGCGGT GTCTAGGGTA	1140
GTGAATCCTG TAAGTTCAAA TTTATGATTA GGTGACGAGT TGACATTGAG ATTGTCTCTT	1200
TCCTGTATCA AAAAATGAAT AAAGCCTTTT TAAACAAAAA AAAAAAAAAA AAAAAAAAAA	1260
AAAAAAAAAA AAAAAA	1276

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

Met Ile Leu Leu Pro Gly Leu Ser His Tyr Asn Ala Leu Gly Leu Phe  
1 5 10 15  
Phe Ala Ala Val Leu Leu Phe Leu Asn Leu Gly Gln Val Pro Met Leu  
20 25 30  
Ala Val Arg Arg Asp Ser Val His Ser Thr Cys Asn Phe Arg Glu Trp  
35 40 45  
Lys

(2) INFORMATION FOR SEQ ID NO:209:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1108 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

GGGGCTCGTC TGTTCAGGA GCCCTGAACC AAAGAGCAGC GGAGTTTGAG AAGCCAGCAG 60  
CTCGGGGTTC GGCAGCAGCG GTCCCATCGG CTGAAGTTTC GGGGGGTGG GGC GCCAGC 120  
GCGCGGGTTC GGGGGGTTC TGGTCTTTGG CTCTCTGACT CGGCTCTGTT TCGACAGCGA 180  
ACATGTCGCG GCCTGTCAGA AATAGGAAGG TTGTTGATTA CTCACAGTTT CAGGAATCTG 240  
ATGATGCAGA TGAAGATTAT GGAAGAGATT CGGGCCCTCC CACTAAGAAA ATTCGATCAT 300  
CTCCCCGAGA AGCTAAAAAT AAGAGGCGAT CTGGAAGAA TTCACAGGAA GATAGTGAGG 360  
ACTCAGAAGA CAAAGATGTG AAGACCAAGA AGGATGATTC TCACTCAGCA GAGGATAGTG 420  
AAGATGAAAA AGAAGATCAT AAAAATGTGC GCCAACAACG GCAGCGCGCA TCTAAGCAG 480  
CTTCTAAACA GAGAGAGATG CTCATGGAAG ATGTGGGCAG TGAGGAAGAA CAAGAAGAGG 540  
AGGATGAGGC ACCATCCAG GAGAAAGATT CCGGCAGCGA TGAAGATTC CTAATGGAAG 600  
ATGATGACGA TAGTGACTAT GGCAGTTCGA AAAAGAAAAA CAAAAGATG GTTAAGAAGT 660  
CCAAACCTGA AAGAAAAGAA AAGAAAATGC CCAAACCCAG ACTAAGGCT ACAGTGACGC 720

CAAGTCCAGT GAAAGGCAAA GGGAAAGTGG GTCGCCCCAC AGCTTCAAAG GCATCAAAGG	780
AAAAGACTCC TTCTCCCAAA GAAGAAGATG AGGAACCGGA AAGCCCGCCA GAAAAGAAAA	840
CATCTACAAG CCCCCCACC GAGAAATCTG GGGATGAAGG GTCTGAAGAT GAAGCCCCCTT	900
CTGGGGAGGA TAAAAGTGA TGATGGTCTG GGGAGAGATT TTATTAAAAA AAAAAAGAAA	960
AAAAAAGAAA AAAGAGGGAG GAAAAAAG AACCTACTTA AGATAGAACA TGGTTTGGC	1020
TATGGCTTGA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	1080
AAAAAAAAA AAAAAAAAAA AAAAAAA	1108

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

Met	Ser	Arg	Pro	Val	Arg	Asn	Arg	Lys	Val	Val	Asp	Tyr	Ser	Gln	Phe
1				5				10					15		
Gln	Glu	Ser	Asp	Asp	Ala	Asp	Glu	Asp	Tyr	Gly	Arg	Asp	Ser	Gly	Pro
			20					25					30		
Pro	Thr	Lys	Lys	Ile	Arg	Ser	Ser	Pro	Arg	Glu	Ala	Lys	Asn	Lys	Arg
			35				40					45			
Arg	Ser	Gly	Lys	Asn	Ser	Gln	Glu	Asp	Ser	Glu	Asp	Ser	Glu	Asp	Lys
	50				55				60						
Asp	Val	Lys	Thr	Lys	Lys	Asp	Asp	Ser	His	Ser	Ala	Glu	Asp	Ser	Glu
65				70					75					80	
Asp	Glu	Lys	Glu	Asp	His	Lys	Asn	Val	Arg	Gln	Gln	Arg	Gln	Ala	Ala
			85					90						95	
Ser	Lys	Ala	Ala	Ser	Lys	Gln	Arg	Glu	Met	Leu	Met	Glu	Asp	Val	Gly
			100					105					110		
Ser	Glu	Glu	Glu	Gln	Glu	Glu	Glu	Asp	Glu	Ala	Pro	Phe	Gln	Glu	Lys
	115						120					125			
Asp	Ser	Gly	Ser	Asp	Glu	Asp	Phe	Leu	Met	Glu	Asp	Asp	Asp	Asp	Ser
	130					135					140				
Asp	Tyr	Gly	Ser	Ser	Lys	Lys	Lys	Asn	Lys	Lys	Met	Val	Lys	Lys	Ser



145		150		155		160
Lys	Pro	Glu	Arg	Lys	Glu	Lys
				Lys	Met	Pro
				Pro	Lys	Pro
				Arg	Leu	Lys
					Ala	
				165	170	175
Thr	Val	Thr	Pro	Ser	Pro	Val
				Lys	Gly	Lys
				Gly	Lys	Val
				Gly	Arg	Pro
				180	185	190
Thr	Ala	Ser	Lys	Ala	Ser	Lys
				Glu	Lys	Thr
				Pro	Ser	Pro
				Pro	Lys	Glu
				Glu		
				195	200	205
Asp	Glu	Glu	Pro	Glu	Ser	Pro
				Pro	Pro	Glu
				Lys	Lys	Thr
				Ser	Thr	Ser
				Pro		
				210	215	220
Pro	Pro	Glu	Lys	Ser	Gly	Asp
				Glu	Gly	Ser
				Glu	Asp	Glu
				Ala	Pro	Ser
				225	230	235
						240
				Gly	Glu	Asp

(2) INFORMATION FOR SEQ ID NO:211:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2952 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

ASTTCRAATT	CGGCCTTCAT	GGMCTAGCAC	GGACTCTGCC	TTCTAAAGT	GGAACCCMC	60
AGTMCCAGCT	GTTGCCTMAG	SGTGGACASA	TCAGSCGAAG	CTCCTGCCCT	GCCTGTTGGC	120
AGCMTCCATG	GGCCAAGCTC	TTGCCTCTCA	CCATCCTCTC	CAGGCCAGT	ACTGTTTCCA	180
GCCGGCCTCT	CCAGGCCCAA	CTCTCCCTCT	CAGCTGTGCC	TGCCGGCCCA	GTCCTACCT	240
CGCAAAAGCC	ACGTTGGGCC	CAGCTCCTGC	CCAGCTCCTG	GCAGCCTTGT	TAAACCCAG	300
GATCCTCTAA	GTCAGGCCTT	TCAGGCCCTG	CCTTTGGCTC	CCCGGTGGCA	TGGAGAGGCC	360
CAGCTCCTGT	CTGACAGCGG	CCTCTCCAGG	CCCAGCTCTT	GCCTCACGTT	GGCCTCCCTG	420
GGCCACGTTT	CCGCTTGCTT	CGCGGCAGCC	CCGACAATCC	CGGCTCCTGC	CTCCCGATGG	480
CATCTTTAGG	CTCATCTCGT	GCCTCACACC	GGCCTGCACC	AGGCACACT	CCTGCCTTTC	540
GGTGGCCTCC	CGCGGCCTGA	CTCCTGCGTC	CCAATGGCCT	CTTTAGGCC	GGCTCGTGCC	600
TCGCGCGCGC	CTCCTGAGGC	CCACCTTTGC	CCTTCTGGCA	GCCTCTCCAG	GCCAGGACT	660
TCCTCAAGTC	GGCCTCTGCC	AGCCCAGTGG	CCGCTCCCG	GCCTCCTCTC	CGGGCCAGC	720

TCCTTGCTCG TGGCTGCGCC CGCGGGCCCA GCTCCTGCCT CTGAACATCC TCCTGTGACT	780
CGGCTCCTGC CCAGCTCCCA GCGGCCTCCG TAGACCCGAA GCCTCCTCCG GTCCAGCTCT	840
CCAGGCCTGC CTCCTGCCTC GTGGCGGCCT TCCCGGCCA TGCTCGTGCC GGCTTCCCGG	900
CAGCCTCCAC GAGCCCGGCT CCTGCCTCAC GCGGGCCCCC CCAGGCCAG CTCGTGCCTC	960
GCGCGGCCT CTCCAGGCC GGCTCCCGCC CAGCCCGACG GCGTCTCCCA GCCCAAGGCT	1020
CCCTTCCTCA ACGTCGGCCC CTCGGGGCCC AGCTCCTGCC TCCCGTGAT GGCCTGTGCG	1080
GGCCACCCG AGGCGGCCCC AAGTCGGCCT CGCCAGGCC AGCTCCTGCC TGGCGTAGGC	1140
CCCTGGGGG ACGGCCTCTG CCCMACAGTG GCCCCTCCG GCCCAGCTCG TGCCCTCGGCT	1200
TGGCGGCCTC AGGCCAGCT CCTGCCTGTG GCGGCCTCT CTCCAGACCC GGCTCTCGCC	1260
TCCCGGCATC CTCCTCAGGC CCAGAGCTGT TTCAGTTGC TAGACCATTT TGTGCTGCTG	1320
CTCGTTCGAC CATCTCCAAG CCCAGCTTTT GCTTTTCTGC AGTTTCTTGA GGCCGAACCTC	1380
CATTTTTCGA ATGGCTTATT TAGGCCAGC TCTTGCCTTT GCATTGTCCC TTCAGGCCCA	1440
GAACCTTTCT ACGTCATCGT CACCAGGCCT AGCTTCTGCA TCTGGTCAGC CTTTAAAGGC	1500
CCAGCTTTTG CCTCATAAAC TCAGCTCCTG TTTAATGGCG GCCTCCCGAG TCCACCTTC	1560
TGCTTCTCTG TGTCCACTCC AGGCCAGCT ACTGCCTTGG TGCTCTTTT AAGTCAATAA	1620
TTTTTTCCAG TCGACCTCTC CAGGCCAAC TTGTACCTCT GAGTGTCTCT TAGGATCTCA	1680
GCTTCTGCCT AACAATGACC TCTTTAGACT CAGCTCATTT TCACTGCTAC ATCTTCAAGC	1740
CATTCTCCTG CCTCTTGCA ACCTCTAGTG GCCCAGCTTC TGCCTCACAG CAGCCTCTCC	1800
ATGCATGCCT AGCTCCTGCC TCTTTAGGGA ACTTACAGGC CTAAACCTTT CTTAATTGG	1860
GCTTCTCAAG CCCAGCTCCT GCCTTCTGTT GGGCTCTACA GGCCTGGCAT CATCCTTTCA	1920
ACAGCCTCTT TAGGCCCGGC CTCCTCAGGA CAAAACATC CTTAAGTCAA CCTCACCAGG	1980
CCCGGCTCCT GTCTCCTTGC GGCTCCTAGA GGCCGAGCTT TTGCCTGCCA ATGGCTCTC	2040
TAGCCCCAGC TTTTGCTGCG CAATGGCCTC TCTAGCCCCA GCTTCTGCCT TTCATCGGTC	2100
TCTCCAGGCT TAGCTCCTTT CTCTTACAGG CCTCTGCAGG CCTAAACCTT CCTCAATTGG	2160
GCATCTCCAG GCCCAGCTCC TGCTCCTCAG CCGCCTCTGC AGGCCTATCT CAAGCCTTAC	2220
AACAGCCTCT TACCCCCAG CTCCTTTCTC CGACTTGTCT CTCAGGCCCT AGAACTTCCT	2280
CATGTTTAC TCACCAGGCC CACCTCCTGC CTCACAGTAG CGTCTACAAG TTTGGCTCCT	2340
GCTTCCCATG GATCTCTCCA GGCCCCAAAC TTTCTCAAGT CAACCTCACC AGGCCCGGCT	2400
TCTCCCTTTC ATCAGCCTTC CAAAGGCCAG CTTTGTGCTT ATGCTCTGCCT TCCGAGTCCC	2460

AGCTCCTGTT TTATGGCAGC CTCCTGAGGC CCAGCTCCTG CCTCCTAGTG GCCTCTTTTG	2520
GCCCAACTCT TTCTCACCA GGGCCTTCCA GACCACGTTT CTGCCTTTTA GCAGCCACTA	2580
CAGGCCCAGC TTTCGCTCCT TTCAAGAGTC CTGCCTCACA GTGGCCTCCC AAGGGCAACT	2640
TTCTGCCTCA TGTCAGCCTC TTGTGCCCTG GTCCTGCTTC CTGGTAGACT CTGCAGGCCC	2700
TGCTCTGCC TTACGTTGCC CCTTTTATAA AGATCCAGTT CCTGCCTCCT GGCTGCCTCT	2760
ATGAGCCCAA ATCCTGCCTA ACAACAACCT GTTTTGGCCC AGCTCCTGCT TCCTGGCAGC	2820
CTCCTTAGGC CAAAAATTTC CTTCAGTTGA CCTCTCCAGG CCCAGCTCCT GCCTCTCAGC	2880
ACCTCTTTA GGCCAGCTC CTGCCTTAAT AAATTGAAT AAATTATTGT TATGTGAAAA	2940
AAAAAAAAAA AA	2952

(2) INFORMATION FOR SEQ ID NO:212:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 73 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

Met Ala Tyr Leu Gly Pro Ala Leu Ala Phe Ala Leu Ser Leu Gln Ala	
1 5 10 15	
Gln Asn Phe Leu Thr Ser Ser Ser Pro Gly Leu Ala Ser Ala Ser Gly	
20 25 30	
Gln Pro Phe Lys Ala Gln Leu Leu Pro His Lys Leu Ser Ser Cys Leu	
35 40 45	
Met Ala Ala Ser Gln Val Pro Pro Ser Ala Phe Leu Cys Pro Leu Gln	
50 55 60	
Ala Gln Leu Leu Pro Trp Cys Ser Phe	
65 70	

(2) INFORMATION FOR SEQ ID NO:213:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1294 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

GTGCCCCGCC GCTGCTGTCA CCCC CGGCCG CTGCTGCCCT CCCCGCCGAG GTTCTACTGC	60
TCTCCTTCTT AAGAAGGGTG GGAGGCACTC GGTCTCTCCC CACACCTCTC GCCTGAGGCC	120
AGGCGCCAGG TGTCGCCTGA AGCCAGACAG CCGGTTTGGG AGCGAGCCTG AGGTCAACCA	180
ATCAATGGCT CAGACAGATA AGCCAACATG CATCCCCCGG GAGCTGCCGA AAATGCTGAA	240
GGAGTTTGCC AAAGCCGCCA TTCGGGCGCA GCCGCAGGAC CTCATCCAGT GGGGGGCCGA	300
TTATTTTGAG GCCTGTCTCC GTGGAGAGAC GCCTCCGGTG AGAGAGCGGT CTGAGCGAGT	360
CGCTTTGTGT AACTGGGCGAG AGCTAACACC TGAGCTGTTA AAGATCCTGC ATTCTCAGGT	420
TGCTGGCAGA CTGATCATCC GTGCAGAGGA GCTGGCCCAG ATGTGGAAAG TGGTGAATCT	480
CCCAACAGAT CTGTTTAATA GTGTGATGAA TGTGGGTCGC TTCACGGAGG AGATCGAGTG	540
GCTGAAGTTT TTAGCCCTTG CTGCGAGCGC TCTGGGAGTT GTAAGTTAGC TTGACTGTTT	600
TTTGTCTCTG AAGGGGAAAT CTCCTCTGCG GCCTGGAAGG GCAGTGCATC TATACACGCG	660
GTCAACTCTG CAGGGCTGAT GATAAACATG CCTCTTCTCC TATTGTCTCT CTCCTCTCTA	720
AAGCAAGGTC ATTTCTGTGC TCGTCAGGCA GTGGCAGGGG TTGGGAGGAG GAGAGAGGGA	780
AACACTGTGG TCAGGCTCTG GGGAGAGTTG ACTACAGTGT AGCTCTTGGA TTATTTATGA	840
ATATTGCCCT CAGATTTATT TTCACTCTGC TCCTTCATT CATATTCCCA GAGACAACCA	900
AGAGCCGACT GTAGAAAAAG ACTTCAGAC ACCTAGAATA TATATCAATA GACACTGTTT	960
AAAAGGGGTA CAATCTTATA GAAAACTATG TAATAACAG AATTGGATGC AGAACTCAGA	1020
CATAAGAAAG CAAAAACAA GAGAGATGAG GCTATTTCTG AATTTAGTCA TGACATCTCC	1080
ATGGATACAG GATGTTTATA CAGATTTATG CCTTTTCCAA ATTTGACTTG TTGTATATTG	1140
GAAAAACAAT TTTACTGTTT TGAAGCCAAA GATGTTGAAA TCAGTTTATA TGTATAGATA	1200
TTTAAAGCTT GGGTATCTTA TATGTGGACT TACATTGTTA AACATTGTTA AAATAAAATG	1260
AATCAAAAAC ATGGTTTTTA AAAAAAAAAA AAAA	1294

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

```
Met Ala Gln Thr Asp Lys Pro Thr Cys Ile Pro Pro Glu Leu Pro Lys
 1             5             10             15

Met Leu Lys Glu Phe Ala Lys Ala Ala Ile Arg Ala Gln Pro Gln Asp
 20             25             30

Leu Ile Gln Trp Gly Ala Asp Tyr Phe Glu Ala Leu Ser Arg Gly Glu
 35             40             45

Thr Pro Pro Val Arg Glu Arg Ser Glu Arg Val Ala Leu Cys Asn Trp
 50             55             60

Ala Glu Leu Thr Pro Glu Leu Leu Lys Ile Leu His Ser Gln Val Ala
 65             70             75             80

Gly Arg Leu Ile Ile Arg Ala Glu Glu Leu Ala Gln Met Trp Lys Val
 85             90             95

Val Asn Leu Pro Thr Asp Leu Phe Asn Ser Val Met Asn Val Gly Arg
100            105            110

Phe Thr Glu Glu Ile Glu Trp Leu Lys Phe Leu Ala Leu Ala Cys Ser
115            120            125

Ala Leu Gly Val Val Ser
130
```

(2) INFORMATION FOR SEQ ID NO:215:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1354 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

```
TTTTTTTTTT TTTTGTATA GCAATGGAAG AATGGCCTCG TACACACGCT AGAGTGGAAA      60
GTCCCAGGCA CCAAGGCTTC CCACCCTAGA AGCAAGCTCA GGGCTTTCTC TTCATCCTTC      120
CAGGGAGAGC ACTGAGAGAT GATGGGGGGT TGGCAGGGGG CATCCCTTGG ATTATCATTC      180
TCCAGACTTA GGCTTGAGAG GGAGGGTGGG GAAGTGGAAT TCTGGGTCTG GTCCACCTCA      240
```

CCTGTTTTCT CAGCTTCTCA CCCACTCAGA GCTCTTGCCC CAATTCTCCC TTTCATCCTG 300  
 CAGATCCCTG CGCCTGACTC ATCTCAGGCG AGGAGGCAAA TCATCAGTTA TCTCAGGCAG 360  
 CAGCAGGACG AGACTCCTTT CTGATTTTCT CTTCCCTGG CCACCTCTCC CCACCCCAT 420  
 TTCACTCATI CCAAACCTCT GGCTCCCCA GCAACTCTAC ATCCTCATCT CCACCTGTTT 480  
 CCTCTCTCGA TGCTGTGGGT GACGTTGGAG AGGGAAGCCC GGAGCCCTGA CCTAGTCCGG 540  
 CGTGAGAGAG GGAATGGAAA CGAGTGTCCT TTTTGAGAAG GCAAATTTAC AGCTGGCTTT 600  
 TGTAATCCTA GCTATTTTTT GTTTGTTTGC TAAGTCTTTG ATAGTCCCCA GTGTGGTTTG 660  
 TCTGCCAGTG ATCTCAGCAC CACCAGAGAG CTTGTTAGAA ATGCGGCATC CCAACCCAC 720  
 CACAGCCCTC CCAAGTCAGA TACTGCCACC TCACGAGGCC CCCAGGGAT CCACAAGTTC 780  
 ATTAAAGTTT CAGGAATCCA ATTCTACTAC AAAATATACA TTTATAATTA GGAAAAGGAT 840  
 AGTTCCTTTA AATGGTAGAA CTTCCCAAT GAGTCAGCTA CCTGTATTTT TGGCTGTCTA 900  
 GGCTAGACAC TGGAGACCAT TCTGCATAGA ATTGTACCTC CTTGAACCTAC TGTTAGGCCT 960  
 TAGGGTGGGG ATTCATCTTT CCCTTCTCCC CACCATGGAG ACAAATCTCT CTAAACATA 1020  
 TCGGGCCCTG GCATGGTGGY TMACGCCTCG GCCTCCCAAA GTTCTGGGAT TACAGGCATG 1080  
 AGCCAYTGTG CCCAGCCACC CGTCACCTGY TAGTGTAGAC AAATGAATAA ACTTAGACAA 1140  
 GCACATGGGC TCCCTCTATA CCAGCCTAGA CTTTGACACT GAAACTCCAT GAGTCTGGGC 1200  
 CACTTCCTGC CACAAGTGTG AATGGAAAAT AAATCATTTT CCAAGGAACC CAAATCACT 1260  
 AAGCCAAGGA GTCAAGTGTG GAACTTTTCA GCAAACCTGC CCCCATTTT ATTTCCTAAA 1320  
 TAAGAGAGCT ACAAGATTA AAAAAAAAAA AAAA 1354

(2) INFORMATION FOR SEQ ID NO:216:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 153 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

Met Glu Ser Ser Val Pro Phe Glu Lys Ala Asn Leu Gln Leu Ala Phe  
 1 5 10 15  
 Val Ile Leu Ala Ile Phe Cys Leu Phe Ala Lys Ser Leu Ile Val Pro

20										25										30																																	
Ser	Val	Val	Cys	Leu	Pro	Val	Ile	Ser	Ala	Pro	Pro	Glu	Ser	Leu	Leu																																						
		35					40					45																																									
Glu	Met	Arg	His	Pro	Asn	Pro	Thr	Thr	Ala	Leu	Pro	Ser	Gln	Ile	Leu																																						
		50				55					60																																										
Pro	Pro	His	Glu	Ala	Pro	Gln	Gly	Ser	Thr	Ser	Ser	Leu	Lys	Phe	Gln																																						
		65			70				75					80																																							
Glu	Ser	Asn	Ser	Thr	Thr	Lys	Tyr	Thr	Phe	Ile	Ile	Arg	Lys	Arg	Ile																																						
				85				90					95																																								
Val	Leu	Leu	Asn	Gly	Arg	Thr	Ser	Pro	Met	Ser	Gln	Leu	Pro	Val	Phe																																						
			100					105					110																																								
Leu	Ala	Cys	Gln	Ala	Arg	His	Trp	Arg	Pro	Phe	Cys	Ile	Glu	Leu	Tyr																																						
		115				120					125																																										
Leu	Pro	Glu	Leu	Leu	Leu	Gly	Leu	Arg	Val	Gly	Ile	His	Leu	Ser	Leu																																						
		130			135						140																																										
Leu	Pro	Thr	Met	Glu	Thr	Lys	Ser	Ser																																													
		145			150																																																

(2) INFORMATION FOR SEQ ID NO:217:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1628 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

CCCCGGTCCC CGCCGAGCC GCTGCATCCT CCGTGCCCGG CCTGAGCTGG AGTCCCCCGC	60
GCCCCCGCG TTCCGCCCG CCATGGCTGC GGTGGCGCTG ATGCCACCGC CGTGCTGTCT	120
GCTGTCTGCT TTGGCGTCGC CGCCCGCCGC CTCGCGCCG TCCGCCCGCG ATCCCTTCGC	180
CCCCAGCTC GGGGACACGC AGAACTGCCA GCTCGGTGC CGCGACCGCG ACCTCGGCC	240
GCAGCCCTCG CAGGCGGGGC TGGAGGGCGC CTCGAGTCT CCCTATGACA GAGCCGTCT	300
GATCAGCGCT TGCAGAGCTG GCTGCCGCCT CTTCTCCATC TCCGATTG TGCCAGAAG	360
CTCCAAGCCC AATGCCACCC AAAGTGAGTG TGAAGCAGCG TCGTGGAAG CCTATGTGAA	420
GGAGGCAGAR CAGCAGGCCT GTAGCCACGG CTGCTGGAGC CAGCCCGCG AGCCTGAGCC	480

GGARCAGAAG AGAAAGGTCC TGGAGGCTCC AAGTGGGGCC CTCTCCCTCT TGGACTTGTT	540
TTCCACCCTC TGCAATGACC TTGTCAACTC AGCCACAGGA TTTGTCTCCT CCACCTGGAC	600
ATACTACTTG CAGACTGACA ATGGGAAAGT GGTGGTGT TT CAGACTCAGC CCATAGTGGA	660
GAGCCTCGGC TTCCAGGGGG GCCGTCTGCA GCGCGTGGAG GTGACCTGGC GAGGCTCCCA	720
CCCTGAAGCC CTGGAGGTGC ACGTGGACCC TGTAGGCCCC CTGGACAAGG TGAGGAAGGC	780
CAAGATCCGA GTCAGACCA GCAGCAAGGC CAAGGTGGAG TCTGAAGAGC CACAGGACAA	840
TGACTTCCTC AGTTGCATGT CCCGGCGCTC GGGTCTGCCT CGCTGGATCC TGGCCTGCTG	900
CCTCTTCCTC TCCGTGCTGG TGATGCTGTG GCTGAGCTGC TCCACCCTGG TGACCGCGCC	960
TGGCCAGCAC CTCAAGTTC AGCCTCTGAC CTTGGAGCAG CACAAGGGCT TCATGATGGA	1020
GCCCGATTGG CCCCTGTACC CGCGCGCTC CCACGCTGT GAGGACAGCC TACCACCCTA	1080
CAAGCTGAAG CTGGACCTGA CCAAGCTGTA GGCCTCCACT GGCCCCATCA CTGCCAACTG	1140
CAGGGGGCCC CTCGGGCCTC ACTTGCCCTG AGCCACAGGAG TCCAAGGGCA GGGTGGGTCC	1200
AGCGTTGAGC CCTCCACCC CCAAATCCTT CCTCTCCTCC CAGTCCACCC CTTGCCCCA	1260
CGGAGTCTCT GGGACGCGT GCGCCAGCTG GGAAGAGGGC GGGATCGGGC ACTGGTTTCT	1320
CCTTGTCCTC GCTTCTCTGG GGGCTTGCTA CTTTCTGCT TCTATTGTGT GGCTTCTGA	1380
GTATTGAAC CCCAGTCTG TGTCACCTTC CTTTCTCCTT CTATGTCCCC TCTCTGCGGG	1440
GGGGCGCTG AGGCTGAGGG GGAGCTGCGT CTGTCTAGGG CTTCCTCCCTT CTCCCCATCC	1500
CGGTCTCCAG AGACCCAGCT TCTGAGAGAC AGGGTGTGGG CATCTCCATG CCCCTATAAA	1560
GCGTGCCTGG GGCCTGTCTG GGGCTGGGGA GGAATAAAC ATGTATATAA AAGAAAAAAA	1620
AAAAAAA	1628

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

Met	Ala	Ala	Val	Ala	Leu	Met	Pro	Pro	Pro	Leu	Leu	Leu	Leu	Leu	Leu
1					5				10					15	





Pro Pro Ser His Ala Cys Glu Asp Ser Leu Pro Pro Tyr Lys Leu Lys  
 325 330 335

Leu Asp Leu Thr Lys Leu  
 340

(2) INFORMATION FOR SEQ ID NO:219:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 671 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

TCGGGCGGCGG GAGTAGCAAG TGGCCATGGG GAGCCTCAGC GGTCGCGCC TGGCAGCAGG	60
AAGCTGTTTT AGGTTATGTG AAAGAGATGT TTCCTCATCT CTAAGGCTTA CCAGAAGCTC	120
TGATTTGAAG AGAATAAATG GATTTTGCAC AAAACCACAG GAAAGTCCCG GAGCTCCATC	180
CCGCACTTAC AACAGAGTGC CTTTACACAA ACCTACGGAT TGGCAGAAAA AGATCCTCAT	240
ATGGTCAGGT CGCTTCAAAA AGGAAGATGA AATCCCAGAG ACTGTCTCGT TGGAGATGCT	300
TGATGCTGCA AAGAACAAGA TGCGAGTGAA GATCAGCTAT CTAATGATTG CCCTGACGST	360
GGTAGGATGC ATCTTCATGG TTATTGAGGG CAAGAAGGCT GCCCAAAGAC ACGAGACTTT	420
AACAAGCTTG AACTTAGAAA AGAAAGCTCG TCTGAAAGAG GAAGCAGCTA TGAAGGCCAA	480
AACAGAGTAG CAGAGGTATC CGTGTGGGCT GGATTTTGAA AATCCAGGAA TTATGTTATA	540
ACGTGCCTGT ATTAAAAAGG ATGTGGTATG AGGATCCATT TCATAAAGTA TGATTTGGCC	600
AAACCTGTAC CATTTCCGTA TTTCTGCTGT AGAAGTAGAA ATAAATTTC TTAATAAAAA	660
AAAAAAAAA A	671

(2) INFORMATION FOR SEQ ID NO:220:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 154 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

Met Gly Ser Leu Ser Gly Leu Arg Leu Ala Ala Gly Ser Cys Phe Arg  
1 5 10 15  
Leu Cys Glu Arg Asp Val Ser Ser Ser Leu Arg Leu Thr Arg Ser Ser  
20 25 30  
Asp Leu Lys Arg Ile Asn Gly Phe Cys Thr Lys Pro Gln Glu Ser Pro  
35 40 45  
Gly Ala Pro Ser Arg Thr Tyr Asn Arg Val Pro Leu His Lys Pro Thr  
50 55 60  
Asp Trp Gln Lys Lys Ile Leu Ile Trp Ser Gly Arg Phe Lys Lys Glu  
65 70 75 80  
Asp Glu Ile Pro Glu Thr Val Ser Leu Glu Met Leu Asp Ala Ala Lys  
85 90 95  
Asn Lys Met Arg Val Lys Ile Ser Tyr Leu Met Ile Ala Leu Thr Val  
100 105 110  
Val Gly Cys Ile Phe Met Val Ile Glu Gly Lys Lys Ala Ala Gln Arg  
115 120 125  
His Glu Thr Leu Thr Ser Leu Asn Leu Glu Lys Lys Ala Arg Leu Lys  
130 135 140  
Glu Glu Ala Ala Met Lys Ala Lys Thr Glu  
145 150

(2) INFORMATION FOR SEQ ID NO:221:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1056 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

CACAAGAGGA GTTACTTGTT CCAGCCTCCT GTGTGGACTG CTTTCCTATC AAAGCACCTT 60  
AGACATGCAC GAGGAAGAAA TATACACCTC TCTTCAGTGG GATAGCCACG CACCAGACAC 120  
TTACCAGAAA TGTCTGTCTT CCAACAAATG TTCAGGAGCA TGCTGTCTTG TGATGTTGAT 180  
TTCATGTGTT TTCTGCATGG GATTATTAAC GGCATCCATT TTCTGGGGCG TCAAGTTGTT 240  
GCAGGTGTCC ACCATTGCGA TGCAGCAGCA AGAAAACTC ATCCAACAAG AGAGGGCACT 300

GCTAAACTTT ACAGAATGGA AGAGAAGCTG TGCCCTTCAG ATGAAATATT GCCAAGCCTT 360  
 CATGCAAAAC TCATTAAGTT CAGGATTTTA TCACTGGCAG CTTGAGGAAG ATTAAAGGAA 420  
 GCTATGATTA CTGGGTGGGG TTGTCTCAGG ATGGACACAG CGGACGCTGG CTTTGGCAAG 480  
 ATGGCTCCTC TCCTTCTCCT GGCCTGTTC CAGCAGAGAG ATCCCAGTCA GCTAACCAAG 540  
 TCTGTGGATA CGTGAAGAGC AATTCCTTC TTTCTGTAA CTGCAGCACG TGAAGTATT 600  
 TTATCTGTGA GAAGTATGCG TTGAGATCCT CTGTCTGAAA GAAATTGTGT TCAAAGTGTT 660  
 CTATTACACT GTTATTTGGA GCATGCCATT GGAAACCCA CCCCCACCC CCCTCAAAAA 720  
 AACAGAACAG TAAACCAAAA TGTGGGCCAT GAAATTAGCA ACCTGGGACT CAATAATACA 780  
 CTTGGGAATA TTCTTCCACA CCGTCCAGAT TTCATTTGAT GTTGTTCACA TTGCAAGAGT 840  
 AAAACTTATT TAGAGCTACA GAAGACAAAA CCCTGAAGAG TTAAGAACAA ACGCAAGGAA 900  
 ATAATTTTTA TTGTTTAAAG CCCGGAATGA CTGTAACTTT CACACAAGGT ACGCATCTAT 960  
 GTTTTGGGG GAGGTGATGT AGTTACAGCT GACTAATATT TTTAAAATAA ATAAATAAAT 1020  
 TTGGCCTTTA AACTCAAAA AAAAAAAAAA AAAAAA 1056

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

Met	His	Glu	Glu	Glu	Ile	Tyr	Thr	Ser	Leu	Gln	Trp	Asp	Ser	Pro	Ala
1				5					10					15	
Pro	Asp	Thr	Tyr	Gln	Lys	Cys	Leu	Ser	Ser	Asn	Lys	Cys	Ser	Gly	Ala
			20					25					30		
Cys	Cys	Leu	Val	Met	Val	Ile	Ser	Cys	Val	Phe	Cys	Met	Gly	Leu	Leu
		35					40				45				
Thr	Ala	Ser	Ile	Phe	Leu	Gly	Val	Lys	Leu	Leu	Gln	Val	Ser	Thr	Ile
		50				55					60				
Ala	Met	Gln	Gln	Gln	Glu	Lys	Leu	Ile	Gln	Gln	Glu	Arg	Ala	Leu	Leu
65					70					75				80	
Asn	Phe	Thr	Glu	Trp	Lys	Arg	Ser	Cys	Ala	Leu	Gln	Met	Lys	Tyr	Cys
				85					90				95		

Gln Ala Phe Met Gln Asn Ser Leu Ser Ser Gly Phe Tyr His Trp Gln  
 100 105 110  
 Leu Glu Glu Asp  
 115

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

ANATTAGATC TGTTCATT TCCAGGCA

29

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

TNGCGTGAGA TCAACTACTC TGCCTGTGA

29

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

ANACAGGACC GAGTCGAGAA GCCAAAGAC

29

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

ANGGGACAAT GCAAACGCAA GAGCTGGGC

29

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

ANGAGGCATG TTTATCATCA GCCCTGCAG

29

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

ANATTTCCT TCTCAAAAGG GACACTGCT

29

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

GNTGGGACTG GGAGGAGAGG AAGGATTG

29

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

GNAACGCCAT AAGCATGTCC TTCTAATGT

29

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

CNTGAAATCA CCATCACAAG ACAGCATGC

29